

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 20, 2005, 16:52:01 ; Search time 7523 Seconds
(without alignments)
10835-240 Million cell updates/sec

Title: US-10-758-979-2
Perfect score: 1434
Sequence: 1 atgaagaagtaatatggtt.....acaatccaagggttcaataa 1434

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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4	597	41.6	609	6	AR395298	AR395298 Sequence
5	526.4	36.7	2460	6	AX416613	AX416613 Sequence
6	523.2	36.5	290242	1	AE017324	AE017324 Listeria
7	518.4	36.2	249050	1	AL596165	AL596165 Listeria
8	518.4	36.2	349980	6	AX417038	AX417038 Sequence
9	518.4	36.2	349980	6	AX417041	AX417041 Sequence
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15	396.2	27.6	1410	6	AX954293	AX954293 Sequence
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C 18	396.2	27.6	110000	1	CP000017_11	Continuation (12 o

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C 23	388.2	27.1	110000	1	CP000056_11	Continuation (12 o
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C 25	233.2	16.3	108759	1	CP000084_12	Continuation (13 o
C 26	227	15.8	110000	1	EX908798_08	Continuation (9 of
C 27	219.6	15.3	110000	1	AP005716_22	Continuation (23 o
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C 41	201.4	14.0	5024	6	AR025183	AR025183 Sequence
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C 45	201.4	14.0	5024	6	BD186432	BD186432 Improved

ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
PUBMED
REFERENCE
AUTHORS

TITLE

JOURNAL
FEATURES
source

gene

AE016952 300029 bp DNA linear BCT 28-MAR-2003
Enterococcus faecalis V583, section 6 of 11 of the complete genome.
AE016952.1 GI:29343605
Enterococcus faecalis V583
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
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Paulsen, I., Banerjee, L., Myers, G.S.A., Nelson, K.E., Seshadri, R.,
Read, T.D., Fouts, D.E., Eisen, J.A., Gill, S.R., Heidelberg, J.F.,
Tettelin, H., Dodson, R.J., Umayam, L., Brinkac, L., Beanan, M.,
Daugherty, S., DeBoy, R.T., Durkin, S., Kolonay, J., Madupu, R.,
Nelson, W., Vamathevan, J., Tran, B., Upton, J., Hansen, T., Shetty, J.,
Khouri, H., Utterback, T., Radune, D., Ketchum, K.A., Dougherty, B.A.
and Fraser, C.M.
Role of Mobile DNA in the Evolution of Vancomycin-Resistant
Enterococcus faecalis
Science 299 (5615), 2071-2074 (2003)
12663927
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Paulsen, I., Banerjee, L., Myers, G.S.A., Nelson, K.E., Seshadri, R.,
Read, T.D., Fouts, D.E., Eisen, J.A., Gill, S.R., Heidelberg, J.F.,
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Khouri, H., Utterback, T., Radune, D., Ketchum, K.A., Dougherty, B.A.
and Fraser, C.M.
Direct Submission
Submitted (03-FEB-2003) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
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DEFINITION
ACCESSION BD193668
VERSION BD193668.1 GI:33003407
KEYWORDS JP 2002529046-A/262.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 5277)
AUTHORS Kunsch, C.A., Dillon, P.J. and Barash, S.C.
TITLE Enterococcus faecalis polynucleotides and polypeptides
JOURNAL Patent: JP 2002529046-A 262 03-SEP-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Unidentified
PN JP 2002529046-A/262
PD 03-SEP-2002
PF 04-MAY-1998 JP 1998548302
PR 06-MAY-1997 US 60/044031, 16-MAY-1997 US 60/046555 PR
14-NOV-1997 US 60/066009
PI CHARLES A KUNSCH, PATRICK J DILLON, STEVEN C BARASH PC
C12N15/31, C07K14/315, C07K16/12, C12Q1/68
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CC Topology: Linear;
CC Enterococcus faecalis polynucleotides and polypeptides FH
Key Location/Qualifiers
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FT source /organism='Unidentified'

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DB	1586	GAACGAGCTTATCGTGAACAGATTGCGAGGATTCCTTTTAAACACTATAGTGTCCGCGCA	1645
QY	601	GAACACGCCAGAGGCGCTTAAATACCTTTTATGATCAAAAACCTCAATCCTATGAAAT	660
DB	1646	GAACACGCCAGAGGCGCTTAAATACCTTTTATGATCAAAAACCTCAATCCTATGAAAT	1705
QY	661	AAGCGTGATTTTCTTATCAGGATCAACAGAGTCATCTGTCCTACTTTTTTAAAGAACGGGA	720
DB	1706	AAGCGTGATTTTCTTATCAGGATCAACAGAGTCATCTGTCCTACTTTTTTAAAGAACGGGA	1765
QY	721	GAACCTTTCGATTTCGCACCATTTGGCAAGAGCTTCGATCTGTGCCTTCTAGCTTAAGTAAA	780
DB	1766	GAACCTTTCGATTTCGCACCATTTGGCAAGAGCTTCGATCTGTGCCTTCTAGCTTAAGTAAA	1825
QY	781	GAACCTTTCAAAAAGAAATTAGCTTTGGCGGACCTTTTACAAATGATCTATAGTGCCTTT	840
DB	1826	GAACCTTTCAAAAAGAAATTAGCTTTGGCGGACCTTTTACAAATGATCTATAGTGCCTTT	1885
QY	841	CCACACAAAAGAGGAGCTATTTCAGAAAAATTTTCGTTATATTCAATCGACAAATGAC	900
DB	1886	CCACACAAAAGAGGAGCTATTTCAGAAAAATTTTCGTTATATTCAATCGACAAATGAC	1945
QY	901	CCAGAAATGTTTGTCAAGTGGCAAAAAGGGGAGACGGGGTACCCCTATAATTGATGCGCA	960

Db	1946	CCAGAAATGTTTGTCAAGTGGCAAAAAGGGGAGACGGGTACCCCTATAATTGATGCGCGCA	2005
Qy	961	ATCGGACAACTGAATCAAACTGGTGGATGCAAAATCGCTTAAAGAAATGATTACTGCTCT	1020
Db	2006	ATCGGACAACTGAATCAAACTGGTGGATGCAAAATCGCTTAAAGAAATGATTACTGCTCT	2065
Qy	1021	TTTTTAGTTAAAAATTTACACATCGATTGGCGTTGGGGTGAANAATACCTTTCAAAAATG	1080
Db	2066	TTTTTAGTTAAAAATTTACACATCGATTGGCGTTGGGGTGAANAATACCTTTCAAAAATG	2125
Qy	1081	TTGATTGACTATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGA	1140
Db	2126	TTGATTGACTATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGA	2185
Qy	1141	ACGGACGCTGCTCCCTTATTTTCGGATTTTTTAATCCAAATTTATCCAGTCAAAAATTTGAT	1200
Db	2186	ACGGACGCTGCTCCCTTATTTTCGGATTTTTTAATCCAAATTTATCCAGTCAAAAATTTGAT	2245
Qy	1201	AATGACGGCGAGTTTCATCAAAAATATGTTTCAGAACTTTAAGCAAGTGCCACAAAAGTAT	1260
Db	2246	AATGACGGCGAGTTTCATCAAAAATATGTTTCAGAACTTTAAGCAAGTGCCACAAAAGTAT	2305
Qy	1261	ATTTCATCAACCAAAATCTAATGAACGAAGCTTTACAAACGCAATATCATGTACATTTAGGA	1320
Db	2306	ATTTCATCAACCAAAATCTAATGAACGAAGCTTTACAAACGCAATATCATGTACATTTAGGA	2365
Qy	1321	GAATAATTCCAAAAACCCATTGTCGATTATGATCAAGTAAATAAACAACATTTGTTCTA	1380
Db	2366	GAATAATTCCAAAAACCCATTGTCGATTATGATCAAGTAAATAAACAACATTTGTTCTA	2425
Qy	1381	TATGAAGCGAGCAAGAAATTTCAATCAAGAAATGAACAATCCAAAGTTTCAATAA	1434
Db	2426	TAKSAGCGAGCAAGAAATTTCAATCAAGAAATGAACAATCCAAAGTTTCAATAA	2479
RESULT 3			
AR395297			
LOCUS	AR395297 966 bp DNA linear PAT 18-DEC-2003		
DEFINITION	Sequence 1312 from patent US 6617156.		
ACCESSION	AR395297		
VERSION	AR395297.1 GI:40123763		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 966)		
AUTHORS	Doucette-Stamm,I.A. and Bush,D.		
TITLE	Nucleic acid and amino acid sequences relating to Enterococcus		
JOURNAL	faecalis for diagnostics and therapeutics		
FEATURES	Patent: US 6617156-A 1312 09-SEP-2003;		
source	Location/Qualifiers		
	1..966		
	/organism="unknown"		
	/mol_type="genomic DNA"		
ORIGIN			
Query Match 65.7%; Score 942; DB 6; Length 966;			
Best Local Similarity 99.9%; Pred. No. 3.9e-174; Mismatches 0; Indels 1; Gaps 1;			
Matches 953; Conservative 0; Mismatches 0; Indels 1; Gaps 1;			
Qy	1	ATGAAAAGAGTAATATGTTTAGACGTTAGCTGATTTACGATTACAGGATAATAAAGCATTAGCA	60
Db	13	ATGAAAAGAGTAATATGTTTAGACGTTAGCTGATTTACGATTACAGGATAATAAAGCATTAGCA	72
Qy	61	CACGCGTTACAAAATCTGCAGCTGATGAATGATTTTATTTATTTCAAAATGAATCCTCAA	120
Db	73	CACGCGTTACAAAATCTGCAGCTGATGAATGATTTTATTTATTTCCAAAATGAATCCTCAA	132
Qy	121	CAATTTATTCAGAAAAGTGCTAATCATACGCTTTTTTTTCGAAAGCTTAGCCTCGTTCAAA	180
Db	133	CAATTTATTCAGAAAAGTGCTAATCATACGCTTTTTTTTCGAAAGCTTAGCCTCGTTCAAA	192
Qy	181	GAACGAATCGATCAAGAGGCACATTTTACAAATCATGTCGCGCAACCATTTAGATTTATTT	240

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Db 193 GAACGAATCGATCAAGAGCAGCATTTTCAATCATGTCGCGGACCACTTAGATTATTT 252
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Qy 241 TCACGTTTGAACGCAATATCCCGATTGGCAGGCCATTATTTTAAATGAAGATCTTGT 300
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Db 253 TCACGTTTGAACGCAATATCCCGATTGGCAGGCCATTATTTTAAATGAAGATCTTGT 312
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Qy 301 GCGTTTGGGCGAAGCGGACCGCAAGCTATGCGCTTTTGAAGAAAATAATATTCAG 360
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Db 313 GCGTTTGGGCGAAGCGGACCGCAAGCTATGCGCTTTTGAAGAAAATAATATTCAG 372
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Qy 361 TCTTTCTCTTTTCAAGATGCGCTTATTTGATGGCTCTGAAGAAATTAAGAAACGATGGC 420
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Db 373 TCTTTCTCTTTTCAAGATGCGCTTATTTGATGGCTCTGAAGAAATTAAGAAACGATGGC 432
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Qy 421 AGCAAGTACCAAGTGTTCACGCCCTATTACAAATAATGGAAGAGCGCCCTAAAGAAACA 480
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Db 433 AGCAAGTACCAAGTGTTCACGCCCTATTACAAATAATGGAAGAGCGCCCTAAAGAAACA 492
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Qy 481 CCGATTCTGTTTCTATACAGCTGAAATAATTTTGTAGTGGGTGCTTTTCCAGAGAG 540
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Db 493 CCGATTCTGTTTCTATACAGCTGAAATAATTTTGTAGTGGGTGCTTTTCCAGAGAG 552
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Qy 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAAACACACTATAGTGTTCGCGGAA 600
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Db 553 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAAACACACTATAGTGTTCGCGGAA 612
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Qy 601 GAAACAGCCAGAGCGCTTAAATACTTTTATGTATCAAAAACTTCAATCCTATGAAAT 660
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Db 613 GAAACAGCCAGAGCGCTTAAATACTTTTATGTATCAAAAACTTCAATCCTATGAAAT 672
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Qy 661 AAGCGTGAATTTCTTTATCAGGATCAACAGGATCATCTGTCTACTTTTAAAGACGGGA 720
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Db 673 AAGCGTGAATTTCTTTATCAGGATCAACAGGATCATCTGTCTACTTTTAAAGACGGGA 732
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Qy 721 GAATCTTCGATTCGCAACCATTTGGCAAGAGCTTGCATCTGCGCTTCTAGCTTAAAGTAAA 780
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Db 733 GAATCTTCGATTCGCAACCATTTGGCAAGAGCTTGCATCTGCGCTTCTAGCTTAAAGTAAA 792
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Qy 781 GAAACCTTCAAAAAAGAATTAGCTTTGGCGGACTTTTCAATATGATCTATAGTCGTTT 840
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Db 793 GAAACCTTCAAAAAAGAATTAGCTTTGGCGGACTTTTCAATATGATCTATAGTCGTTT 852
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Qy 841 CCACAAACAAAAGAGAGAGCTATTCAGAAAAATTTTCGTTTATTCATGGAACAAATGAC 900
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Db 853 CCACAAACAAAAGAGAGAGCTATTCAGAAAAATTTTCGTTTATTCATGGAACAAATGAC 912
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Qy 901 CCAGAAATCTTTCTCAAGTGGCAAAAAGGGGAGAC-GGGGTACCTTATAATTGA 953
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Db 913 CCAGAAATCTTTCTCAAGTGGCAAAAAGGGGAGACGGGGGTACCTTATAANTGA 966

RESULT 4
AR395298 609 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 1313 from patent US 6617156.
ACCESSION AR395298
VERSION AR395298.1 GI:40123765
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

Unknown.
Unclassified.
1 (bases 1 to 609)
Doucette-Stamm,L.A. and Bush,D.
Nucleic acid and amino acid sequences relating to Enterococcus
faecalis for diagnostics and therapeutics
Patent: US 6617156-A 1313 09-SEP-2003;
Location/Qualifiers
1. .609
/organism="unknown"
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Query Match 41.6%; Score 597; DB 6; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.4e-106;
Matches 608; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 827 TCTATAGTGGTTTCCACAAACAAAGAGAGAGCTATTTCAGRAAAATTTTCGTTATATTC 886
Db 1 TCTATAGTGGTTTCCACAAACAAAGAGAGAGCTATTTCAGRAAAATTTTCGTTATATTC 60
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Qy 887 AATGAGCAAAATGACCCAGAAATGTTTCTCAAGTGGCAAAAAGGGGAGAC-GGGGTACCCCT 945
Db 61 AATGAGCAAAATGACCCAGAAATGTTTCTCAAGTGGCAAAAAGGGGAGACGGGGTACCCCT 120
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Qy 946 ATAAATTGATGCGCAATGCGACAACTGAATCAAACTGGTGGATGCAATTCGCTTAAGA 1005
Db 121 ATAAATTGATGCGCAATGCGACAACTGAATCAAACTGGTGGATGCAATTCGCTTAAGA 180
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Qy 1006 ATGATTAATGCTCTTTTGTAGTTAAATAATTTACACATCGATTCGCGGTGGGGTGAATAA 1065
Db 181 ATGATTAATGCTCTTTTGTAGTTAAATAATTTACACATCGATTCGCGGTGGGGTGAATAA 240
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Qy 1066 TACTTTCAAAAAATGTTGATTGACTATGCTGCCAATAATATCGGTGGCTGGCAATGG 1125
Db 241 TACTTTCAAAAAATGTTGATTGACTATGCTGCCAATAATATCGGTGGCTGGCAATGG 300
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Qy 1126 GCTGCTTCAACAGAGACGGAGCGTGTCCCTTATTTTCGGATTTTAAATTCGAATTCAG 1185
Db 301 GCTGCTTCAACAGAGACGGAGCGTGTCCCTTATTTTCGGATTTTAAATTCGAATTCAG 360
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Qy 1186 TCAAAAAAATTTGATATGACGGCGAGTTTCATCAAAAAATATGTTCCAGAACTTTAAGCAA 1245
Db 361 TCAAAAAAATTTGATATGACGGCGAGTTTCATCAAAAAATATGTTCCAGAACTTTAAGCAA 420
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Qy 1246 GTGCCACAAAAGTATATTTCATCAACCAAACTCTAATGAACGAAGCCTTACAAACGCAATAT 1305
Db 421 GTGCCACAAAAGTATATTTCATCAACCAAACTCTAATGAACGAAGCCTTACAAACGCAATAT 480
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Qy 1306 CATGTACATTTAGGAGAAAAATTTTCAAAACCCCAATTTGCGATTATGCAATCAAGTAAATAA 1365
Db 481 CATGTACATTTAGGAGAAAAATTTTCAAAACCCCAATTTGCGATTATGCAATCAAGTAAATAA 540
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Qy 1366 CAACATTTTCTATATGAAGCGAGCAGCAAAATTTTCATCAAGAAATTCATCAAGAAATTCACCAAGG 1425
Db 541 CAACATTTTCTATATGAAGCGAGCAGCAAAATTTTCATCAAGAAATTCATCAAGAAATTCACCAAGG 600
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Qy 1426 TTTCAATAA 1434
Db 601 TTTCAATAA 609
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RESULT 5
AX416613 2460 bp DNA linear PAT 02-SEP-2002
LOCUS
DEFINITION Sequence 3604 from Patent WO0228891.
ACCESSION AX416613
VERSION AX416613.1 GI:21449070
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN

Listeria monocytogenes ATCC 19115
Listeria monocytogenes ATCC 19115
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
1
Kunst,F. and Glaser,P.
Listeria inocua, genome and applications
Patent: WO 0228891-A 3604 11-APR-2002;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)
Location/Qualifiers
1. .2460
/organism="Listeria monocytogenes ATCC 19115"
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/db_xref="taxon:176281"

Best Local Similarity 61.6%; Pred. No. 6.2e-93;		Matches 883; Conservative 0; Mismatches 536; Indels 15; Gaps 2;	
Qy	1	ATGAAAAGAGTAATATGCTTTAGACGTGATTTACGATTTACAGGATAATAAGCAATTAGCA	60
Db	241	ATGACTTCGGTAAATGTGTTTTCGGAGAGATCTTCGAGTAAACGATATAAAGCTCTCTAT	300
Qy	61	CACGGTTACAAAATTCGACCTGATGAATGATTTATTTATTTCCAAATGAATCCTCAA	120
Db	301	CATGC-----TTGTAAGAGAGACGATTTGCTTTTGTATTATTCGAAGTAATCCACGA	351
Qy	121	CAATTTATTCAAGAAAGTGCTAATCATAAACGTTTTTTTTTGCAAGCTTAGCCTCGTCAAA	180
Db	352	CAGTTTCATCAGAGAGTCTTAGCCACCAAGCTTTTTTTGCAAGTGTGGCTCATTTAAG	411
Qy	181	GAAAGAAATCGATCAAGAGGCAATTTACAAATCATGTCGCGCAACCAATTAGATTTATTT	240
Db	412	CAAGAAATCGATAAACTGCGCATTTTACAAATCATGTTTGGTGAACCGATAGATGCTTC	471
Qy	241	TCACGTTTGAACCGCAATTTACCCGATTTGGCAGGCCATTTATTTATTAATGAAGTACTTGT	300
Db	472	CAACAACATTAAGAGTTTCGTTACCAAGCTGGGATAAAGTTTATTTCAACCGGTGATGAACA	531
Qy	301	GGCTTTGGGCAAAAGCGGACAGCAAGCTATGCGCTTTTTTTGAAGAAATAATATTTCAG	360
Db	532	GGATACGAGCAAGCGGAGTAGCGCGCGCAAGGTTCTTTTGACGAACAATAATCGAG	591
Qy	361	TCCTTTCTCTTTCAAGATGCGCTATTTGCATGGCTCTGAAGAAATTTAAGAAACGATGGC	420
Db	592	GTTCAAGCTTTCCAGATAGCTATCTTCAATTCAGCGGAAGAGTAAAGAAATCTCCAACA	651
Qy	421	AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAATGGAAGAGCGCCCTAAGAAACA	480
Db	652	GAATACTATAAAATTTTACCCTTATTATATAAAATGCGCGAAGAAATAAAGAAACG	711
Qy	481	CCGATTCTGTTTCTCTATACAGCTGMAAAATTTTTTAGTGCGTGTCTTTTCCAGAAGAG	540
Db	712	CCGTTCAAGATGACTTTTAAGCATGAGNATATCCGAAGAAGAACTGTTTCTCAATAT	771
Qy	541	GAACAGCTTATCGTGAAACAGATTGCGAGGATTCCTTTAACACACTATAGTGTCCGCGAA	600
Db	772	GAAGAACAATTTGCGGAATGACT-----AGCGATTTACCGATATTAGATATTGTTGAA	825
Qy	601	GAAACAGCAGAGCGCTTAAATACTTTTATTGATCAAAACTTCAATCCTATGAAT	660
Db	826	CGACAGCGAAACACGAGACTTTCGGAATTTTATAAACAACGATGTGCTGACTATGACAAA	885
Qy	661	AAGCGTGATTTTCCTTATCAGGATCAACAGAGTCTGCTACTTTTAAAGAACGGGA	720
Db	886	CGGAGAGATTTCCCGAACTGGATATAACAAGCCATTTATCACGTTATTACGAACCGGG	945
Qy	721	GAACTTCGATTCGCACCATTTGGCAAGAGCTTGCACTGTGCGCTTCTAGCTTTAAGTAAA	780
Db	946	GAAATCTCGATTCGACGATTTGGCAGACACTTCAAGAAACAGAAAGCAAGAGGACGA	1005
Qy	781	GAAACCTTCAAAAAGATTTAGCTTGGCGCACTTTTACATATATGATCTAGTGCCTTT	840
Db	1006	GCTACATTTGAAAAGAACTGTGTAGGCGCACTTTTATAATATGATTTAGTTTCTTTT	1065
Qy	841	CCACAACAAAAGAGGAGCTATTCAAGAAAAATTTTCGTTATATTTCATGAGCAAAATGAC	900
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Qy	901	CCAGAAATGTTTGTCAAGTGGCAAAAAGGGAGACGGGGTACCCCTATAATTTGATGCCGCA	960
Db	1126	CGCGAATATTTCAAAGCGTGGCAAGAGGGAAGACTGGTTTTCCCGCTCGTTGATGCGGCG	1185
Qy	961	ATGCGAACAATGAATCAAACTGGTTGGATGCAAAATCGCTTTAAGAAATGATTACTGCCCTCT	1020
Db	1186	ATGCCCAAGTTGAAGAAACACTGGTTGGATGCATAATCGACTAAGAATGATTACGCGCTCC	1245
Qy	1021	TTTTTAGTAAAAATTTACACATCGATTGGCGTTGGGTGAAAAATACTTTTCAAAAAATG	1080

Db	1246	TTTTTAACAAAAAGATTGTGCTGATTGATTGGCGTTTTTGGCGAAAAAGTAGTATTTTCAACAAATG	1305
Qy	1081	TTGATTGACTATGATGCTGCCAATAATATATCGTGGCTGGCAATGGGCTGCTTCAACAGGA	1140
Db	1306	CTGATTGATTATGATCTCGAGTAATATTGGTGGCTGGCAATGGGCGGCTTCGACTGGA	1365
Qy	1141	ACGAGCGCTGCTCCTTATTTTTCGGATTTTAAATCCAAATTTCCAGTCAAAAAATTTTGT	1200
Db	1366	ACGATGCGGTGCATATCTTTAGGATTTTCAACCAACGACACATCACAAAAATTTTGT	1425
Qy	1201	AATGACGGCCAGTTCATCAAAAAATATGTTTCCAGAATTTAAGCAAGTCCACAAAAGTAT	1260
Db	1426	TCGACTGGGAAATTTATTCGAAAAATATGTAAGAGAGTTAGCGAATCTACCTGATAAATAT	1485
Qy	1261	ATTATCAACCAAAATCTAATGAACGAGCCCTTACAAACGCAATATCATGTACATTTAGGA	1320
Db	1486	ATTATCAACCAAAAAATGTGAGAACTGAGCAGAAAGAGCATGGCTTGTCTGTAGGA	1545
Qy	1321	GAAAAATATCCAAACCCATTGTCGATTATGTCATCAAGTAAAAAACAACATTTGTTTCTA	1380
Db	1546	AAAGACTATCCATTTCCGATAGTTGACCATAAAGACGCGGAATTTAGCCATTTGCACGC	1605
Qy	1381	TATGAACGCGACGAAGAAATTCATCAAGAAATGAACAATCCAAGTTTCAATAA	1434
Db	1606	TACGAGTTTAGCAAGAGCATTCTAGGGAAATATATAGATAANTAGTCAATCA	1659
RESULT 6			
LOCUS	AE017324	290242 bp	DNA linear BCT 30-APR-2004
DEFINITION	Listeria monocytogenes str. 4b F2365, section 3 of 10 of the complete genome.		
ACCESSION	AE017324	AE017262	
VERSION	AE017324.1	GI:46880047	
KEYWORDS	Listeria monocytogenes str. 4b F2365		
SOURCE	Listeria monocytogenes str. 4b F2365		
ORGANISM	Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.		
REFERENCE	1 (bases 1 to 290242)		
AUTHORS	Nelson, K.E., Fouts, D.E., Mongodin, E.F., Ravel, J., DeBoy, R.T., Kolonay, J.F., Rasko, D.A., Angiuoli, S., Gill, S.R., Paulsen, I.T., Peterson, J.D., White, O., Nelson, W.C., Nierman, W.C., Beanan, M.J., Brinkac, L.M., Daugherty, S.C., Dodson, R.J., Durkin, A.S., Madupu, R., Haft, D.H., Selengut, J., Van Aken, S., Khouri, H., Fedorova, N., Forberger, H.A., Tran, B., Kacharion, S., Wondolring, L.D., Uhlrich, G.A., Bayles, D.O., Luchansky, J.B. and Fraser, C.M.		
TITLE	Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen Listeria monocytogenes reveal new insights into the core genome components of this species		
JOURNAL	Nucleic Acids Res. 32 (8), 2386-2395 (2004)		
PUBMED	15115801		
REFERENCE	2 (bases 1 to 290242)		
AUTHORS	Nelson, K.E., Fouts, D.E., Mongodin, E.F., Ravel, J., DeBoy, R.T., Rasko, D.A., Kolonay, J.F., Angiuoli, S., Gill, S.R., Paulsen, I.T., Peterson, J.D., White, O., Nelson, W.C., Nierman, W.C., Van Aken, S.E., Khouri, H.M., Fedorova, N.B., Forberger, H.A., Tran, B. and Fraser, C.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-FEB-2004) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA		
FEATURES	Location/Qualifiers		
source	1. .290242		
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gene	/db_xref="taxon:265669"		
	83. .1354		
	/locus_tag="LMOF2365_0566"		
CDS	83. .1354		
	/locus_tag="LMOF2365_0566"		
	/note="identified by similarity to SP:Q01264; match to protein family HMM PF01546; match to protein family HMM TIGR01879"		
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Ds	54185	CAAGAAATCGATAAAACCTGCGCAATTTACAAATCATGTTTGTGTAACCGATAGAATGCTC 54244	
Qy	241	TCAGTTTGAACGCAAAATACCCGATGGCAGGCCATTTATTTTATGAAGATACTTGT 300	
Ds	54245	CAACAACATTAAGATTTCGCTACCAAGCTGGGATAAAGTTTATTTCAACCGTGATGAACA 54304	
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Qy	361	TCCTTTCTTTTCAAGATGCCTATTATTCATGGCTCTGAAGAAATAAGAAAGCATGGC 420	
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Ds	54659	CGGAGAGATTTCCCGAATCGATAAACAAGCCATTATACCGTTATTACGACGGGG 54718	
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Ds	54719	GAAATCTCGATTCCGACGATTTGGCAGTCACTTCAAGAAACAGAAGCAACAGAAGGACGA 54778	
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Ds	54839	CCTAACCAAAAAACGAGCCGATCCAGAAAAATTATTCGTTTTTATGAATGGAAAAATAAC 54898	
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RESULT 7	AL596165	249050 bp	DNA	linear	BCT 16-APR-2005
LOCUS	Listeria innocua Clp11262	complete genome	segment 3/12.		
DEFINITION	AL596165	AL592022			
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VERSION					
KEYWORDS					
SOURCE	Listeria innocua				
ORGANISM	Listeria innocua				
REFERENCE	1	Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.			
AUTHORS	Glaser, P., Frangeul, L., Buchrieser, C., Rueniok, C., Amend, A., Baquero, F., Berche, P., Bloeker, H., Brandt, P., Chakraborty, T., Charbit, A., Chetouani, F., Couve, E., de Daruvar, A., Dehoux, P., Domann, E., Dominguez-Bernal, G., Duchaud, E., Durant, L., Dussurget, O., Entian, K.D., Fsihi, H., Garcia-del Portillo, F., Garrido, P., Gautier, L., Goebel, W., Gomez-Lopez, N., Hain, T., Hauf, J., Jackson, D., Jones, L.M., Kaerst, U., Kreft, J., Kuhn, M., Kunst, F., Kurapkak, G., Madueno, E., Maitournam, A., Vicente, J.M., Ng, E., Nedjari, H., Nordsiek, G., Novella, S., de Pablo, B., Perez-Diaz, J.C., Purcell, R., Remmel, B., Rose, M., Schluster, T., Simoes, N., Tierrez, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and Cosset, P.				
TITLE	Comparative genomics of Listeria species				
JOURNAL	Science 294 (5543), 849-852 (2001)				
PUBMED	11679669				
REFERENCE	2	(bases 1 to 249050)			
AUTHORS	Glaser, P., Frangeul, L. and Rueniok, C.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-JUL-2001) Glaser P., Institut Pasteur, Genomique des Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE				
COMMENT	E-mail: pglaser@pasteur.fr Phone: +33 (0)1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.				

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RESULT 8

AX417038	AX417038	349980 bp	DNA	linear	PAT 02-SEP-2002
LOCUS					
DEFINITION	Sequence 4029 from Patent WO0228891.				
ACCESSION	AX417038				
VERSION	AX417038.1	GI:21449648			
KEYWORDS					
SOURCE	Listeria innocua				
ORGANISM	Listeria innocua				
REFERENCE	1 Kunst, F. and Glaser, P.				
AUTHORS	Listeria innocua, Genome and applications				
TITLE	Patent: WO 0228891-A 4029 11-APR-2002;				
JOURNAL	INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE				
FEATURES	SCIENTIFIQUE (CNRS) (FR)				
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Query Match 36.2%; Score 518.4; DB 6; Length 349980;
Best Local Similarity 61.2%; Pred. No. 5.1e-92;
Matches 878; Conservative 0; Mismatches 541; Indels 15; Gaps 2;

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AX417041
LOCUS AX417041 349980 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 4032 from Patent WO0228891.
ACCESSION AX417041
VERSION AX417041.1 GI:21449651
KEYWORDS Listeria innocua
SOURCE Listeria innocua
ORGANISM Listeria innocua
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE

1 Kunst, F. and Glaeser, P.
Listeria innocua, genome and applications
Patent: WO 0228891-A 4032 11-APR-2002;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)

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seq 4034: 0.900.001 to 1.249.980
seq 4035: 1.200.001 to 1.549.980
seq 4036: 1.500.001 to 1.849.980
seq 4037: 1.800.001 to 2.149.980
seq 4038: 2.100.001 to 2.449.980
seq 4039: 2.400.001 to 2.749.980
seq 4040: 2.700.001 to 3.049.980
seq 4041: 3.000.001 to 3.011.208"

ORIGIN

Query Match 36.2%; Score 518.4; DB 6; Length 349980;
Best Local Similarity 61.2%; Pred. No. 5.1e-92;
Matches 878; Conservative 0; Mismatches 541; Indels 15; Gaps 2;

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RESULT 10
AX417042 349980 bp DNA linear PAT 02-SEP-2002
LOCUS
DEFINITION Sequence 4033 from Patent WO0228891.
ACCESSION AX417042
VERSION AX417042.1 GI:21449652
KEYWORDS
SOURCE Listeria innocua
ORGANISM Listeria innocua
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE 1
AUTHORS Kunst, F. and Glaser, P.
TITLE Listeria innocua, Genome and applications
JOURNAL Patent: WO 0228891-A 4033 11-APR-2002;
INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)
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seq 4032: 0.300.001 to 0.649.980
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seq 4034: 0.900.001 to 1.249.980
seq 4035: 1.200.001 to 1.549.980
seq 4036: 1.500.001 to 1.849.980
seq 4037: 1.800.001 to 2.149.980
seq 4038: 2.100.001 to 2.449.980
seq 4039: 2.400.001 to 2.749.980
seq 4040: 2.700.001 to 3.049.980
seq 4041: 3.000.001 to 3.011.208"

ORIGIN

Query Match 36.2%; Score 518.4; DB 6; Length 349980;
Best Local Similarity 61.2%; Pred. No. 5.1e-92;
Matches 878; Conservative 0; Mismatches 541; Indels 15; Gaps 2;

Qy 1 ATGAAAGAGTATATGTTTAGACGTGATTACGATTACAGATTAATAAGCATTAGCA 60
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VERSION AL591975.1 GI:16409709			
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TITLE Comparative genomics of Listeria species			
JOURNAL Science 294 (5543), 849-852 (2001)			
PUBMED 11679669			
REFERENCE 2 (bases 1 to 280050)			
AUTHORS Glaser, P., Frangeul, L. and Ruiniok, C.			
TITLE Direct Submission			
JOURNAL Submitted (06-JUN-2001) Glaser P., Institut Pasteur, Genomique des Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE			
COMMENT E-mail: pglaser@pasteur.fr			
Phone: +33 1 45 68 89 96, Fax: +33 (0) 1 45 68 87 86.			
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Best Local Similarity			
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DEFINITION Sequence 2856 from Patent WO0101118.
ACCESSION AX641666

VERSION AX641666.1 GI:28474427
KEYWORDS

SOURCE Listeria monocytogenes

ORGANISM Listeria monocytogenes

REFERENCE 1 Bacteria, Firmicutes; Bacillales; Listeriaceae; Listeria.

AUTHORS

Buchrieser, C., Frangeul, L., Couve, E., Rusniok, C., Feihi, H.,
Dehoux, P., Dussurget, O., Chetouani, F., Nedjari, H., Glaser, P.,
Kunst, F., Cossart, P., Daniels, J., Goebel, W., Kref, J., Kuhn, M.,
Ng, E., Vasquez-Boland, J., Dominguez-Bernal, G., Garrido-Garcia, P.,
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Garcia del Portillo, F., Gomez-Lopez, N., Madueno, E., de Pablo, B.,
Wehland, J., Kaerst, U., Entian, K. D., Hauf, J., Rose, M. and Voss, H.
Listeria monocytogenes genome, polyptides and uses
Patent: WO 0101118-A 2856 11-APR-2001;
INSTITUT PASTEUR (FR)

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AUTHORS Kunst,F. and Glaser,P.
TITLE Listeria innocua, genome and applications
JOURNAL Patent: WO 0228891-A 1690 11-APR-2002;
INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
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TITLE		Patent: WO 03093306-A 1139 13-NOV-2003;
JOURNAL		Chiron SRL (IT); THE INSTITUTE FOR GENOMIC RESEARCH (US)
FEATURES		Location/Qualifiers
source		1..1410
		/organism="Streptococcus pyogenes"
		/mol_type="unassigned DNA"
		/db_xref="taxon:1314"
ORIGIN		
Query Match	27.6%;	Score 396.2; DB 6; Length 1410;
Best Local Similarity	55.9%;	Pred. No. 2.2e-67;
Matches	777; Conservative	0; Mismatches 608; Indels 6; Gaps 1;
Qy	9	AGTAATATGTTTGTAGAGCTGATTTACGATTACAGGATAATAAGCAATTAGCACACGCGTT 68
Db	9	AGTATGCTGGTTTCGTAGAGATTTAAGGATTGATGATCAAAAGCTTTAGCTCATGCTAT 68
Qy	69	ACAAAATCTGACAGCTGATGAATTTTATTTATTTCCAAAATGAATCCTCACAATTTAT 128
Db	69	TGCTAGTCAATCAACCAACCTTATGTGTGTTTCAATTTTAAACAGGAGCAATTTAAATCTGCT 128
Qy	129	TCAGAAAGTGCTTAATCATAAACGCTTTTGTGCAAGCTTAGCCTCGTTCAAGAACGAAT 188
Db	129	ACATAGTCGGAATCAATCTAGTTTATTTACTAGCGTTTGTGGCTTTTAGAANGTTATTAAA 188
Qy	189	CGATCAAGAGGCACTTTACAAATCATGTGCGCGAACCACTTAGATTTATTTTTCACGTTT 248
Db	189	ATGTGAAGGTATTGACTTTATCTAATGATGAGACTTAATGACCTGTTTGTGAGCAATT 248
Qy	249	GAAACGCAAAATTAACCGATTGGCAGGCCATTTATTTTATGAAGATACCTTGTGCTTTGG 308
Db	249	ATTGACACAAATTTAAAAGACTGGACAGATGTGTTTAACTATGATGAATCTGGATATGG 308
Qy	309	GGCAAGCGGACGACGACAGCTATGCGCTTTTGTGAAGAAATAATTTTTCAGTCTTTCTC 368
Db	309	TCGTTTACGTGATCAAAAAGCAGCAAAATTTTCAAAAAAATGCGATCTGTTCTATAC 368
Qy	369	TTTTCAAGATGCCCTATTGTCATGGCTCTGAAGAAATTTAAGAAAGACGATGGCAGCAAGTA 428
Db	369	CTACCAAGACTCACTATTATCATGCTAGTCAAGAGATCATTTAACCAATCAGTCAAGCCTTA 428
Qy	429	CCAAGTGTTTACGCCCTATTACAATAATGGAAGAGCGCCCTAAAGAAACACCGATTC 488
Db	429	TAAAGTGTTTTACGCCCTACTATAGGATTTGGCAAAATTTATCCGAAAGAGACTCCTATTAA 488
Qy	489	TGTTTCTCTATACAGCTGMAAAATTTTATAGTGGTGTCTTTTCCAGAGAGGAGCAGC 548
Db	489	AGTAGAACTATCCGAAGGCGAGGTGGTTAAA-----TCITGAGACACCAAGATGTTTT 542
Qy	549	TTATCGTGAACAGATTGCGAGGATTCCTTTTAAACACTATAGTGTGCGCGAAGAAACAGC 608
Db	543	AAGGACTGTTGAGAGTTTTAAGATGAAATAATCAGGATGTTGCAACTTTTGTATGAAGC 602
Qy	609	CAGAAGCGCTTAAATACITTTTATGATCAAAACTTTCAATCTCTATGAAATTAAGCGTGA 668
Db	603	GTCAAAACAACTAAATCGATTTATTCAAGACCAATTAGCAGCTTATCACGCTTAATCGAGA 662
Qy	669	TTTTTCTTATCAGGATCAACAGGATCATCTGTCTACTTTTAAAGAACGGGAGAACTTTC 728
Db	663	TTTTTCAGCGCAGCTAGGACGAGTCCGTTGTCTCTCTTTTAAAGAAATAGAGCTATTGG 722
Qy	729	GATTTCGACCATTTGGCAAGAGCTTGCATCTGTGCTCTTCTAGCTTAAAGTAAAGAAACCTT 788
Db	723	CATTGCGACGGTATATCACGCTGCTGCTCAAGCACCAATAGTCTAGGCGAAGCTACTTT 782
Qy	789	CAAAAAGAAATTAGTGTGGCGGACTTTTACAATATGATCTATAGTGGCGTTTCCACAACA 848
Db	783	TTTTAAAGAAATTAGCTTGGAGAGACTTTTACAATATGCTATGTGCTTATCTCTGATCA 842

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 20, 2005, 17:33:07 : Search time 6266 Seconds
(without alignments)
10707.417 Million cell updates/sec

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Perfect score: 1434
Sequence: 1 atgaaagagtaatatggtt.....acaatccaaggtttcaataa 1434

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
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5: gb_est4:*
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7: gb_est6:*
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10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	166	11.6	544	2	BI263965 NF092B05P
C 2	156.4	10.9	823	10	CL659411 PRI0134a
C 3	145.4	10.1	841	10	C2547170 SRAA-aad7
C 4	138.2	9.6	434	2	BE459864 EST415156
C 5	137.4	9.6	760	8	DT043899 polyA9-H6
C 6	129	9.0	989	11	AL425181 clone BA0
C 7	116.8	8.1	787	8	DN981737 SV6_40804
C 8	113.2	7.9	740	6	CD458345 Fg08_1210
C 9	111.6	7.8	991	11	AL425355 clone BA0
C 10	108.2	7.5	1063	9	BZ563216 pac82-164
C 11	107.6	7.5	773	10	CL692005 PRI0157d
C 12	106.8	7.4	420	9	BZ893625 HL5_0136
C 13	104.8	7.3	717	8	DT001226 Mdr1a1012
C 14	104.6	7.3	748	3	BI311349 EST531309
C 15	103.6	7.2	699	5	BO854812 QGB24E15
C 16	102.4	7.1	649	6	CA989448 EST642956
C 17	101	7.0	427	7	CO142739 EST937410
C 18	100.8	7.0	393	7	CO067931 Mdfrc3028
C 19	99.6	6.9	854	8	CV769258 FGAS06364
C 20	99.4	6.9	645	6	CD924582 G750_113J
C 21	97.8	6.8	528	7	CN491610 Mdfw2005k
C 22	97	6.8	1071	4	CNS0A821 Arabidops

23	96.4	6.7	615	1	AW309100
24	94	6.6	449	7	COL13296
25	92.2	6.4	798	8	CX7114323
26	91.8	6.4	619	5	BQ392047 NISC_hg22
27	91.4	6.4	526	7	CO901104 Mdfrc3066
28	90.8	6.3	733	5	BQ862562 QGC21624
29	90.2	6.3	607	8	CX487760 JGI_X2G29
30	90.2	6.3	627	8	CX487761 JGI_X2G29
31	89.8	6.3	795	8	CX471210 JGI_X2G48
32	89.8	6.3	552	3	BI787441 sai45g09
33	89.2	6.2	601	5	BU082486 saq33c04
34	89.2	6.2	723	5	BQ863292 QGC23H21
35	89.2	6.2	773	5	BQ861871 QGC19M24
36	88.2	6.2	692	7	CV532994 LVS_032_G
37	87.6	6.1	906	5	BU916216 AGENCOURT
38	87.2	6.1	654	2	BE249224 BE024D05D
39	87.2	6.1	690	2	BF631699 NF007A12D
40	87	6.1	791	6	CB671067 OSJNEe04J
41	87	6.1	792	6	CB671155 OSJNEe04H
42	87	6.1	803	6	CB677310 OSJNEe14B
43	86.5	6.0	825	6	CA765778 AFS3-Rpf
44	86.5	6.0	696	5	BQ860163 QGC15A06
45	85.2	5.9	600	9	BZ893135 HL11_0181

ALIGNMENTS

RESULT 1
BI263965/c

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BI263965 544 bp mRNA linear EST 18-JUL-2001
clone NF092B05PL1F1045 Phosphate starved leaf Medicago truncatula cDNA
clone NF092B05PL 5', mRNA sequence.

BI263965
BI263965.1 GI:14865752

EST

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosoidae I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 544)

Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,

Flores, H.R., Imman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula phosphate-starved leaf library

Unpublished (2000)

Contact: Harrison MJ

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7325

Fax: 580 221 7380

Email: mjharrison@noble.org

Insert Length: 544 Std Error: 0.00

Plate: 092 row: B column: 05

Seq primer: TCACACGGAACACGCTATGAC.

Location/Qualifiers

1..544

/organism="Medicago truncatula"

/mol_type="mRNA"

/db_xref="taxon:3880"

/clone="NF092B05PL"

/tissue_type="leaf"

/dev_stage="trifoliolate"

/note="Vector: Lambda Zap; At the trifoliolate stage, M.

truncatula plants were transplanted to phosphate-free sand

and grown for a further 30 days. During this 30 day

period, the plants were fertilized twice weekly with 1/2

Hoaglands solution containing only 20uM potassium

phosphate. RNA was prepared from above ground tissues."


```

RESULT 7
DN981737/c
LOCUS
DEFINITION
SV6 40E04_AV59_023 SV6 Solanum chacoense cDNA, mRNA linear EST 15-JUN-2005
ACCESSION
DN981737
VERSION
DN981737.1 GI:67769548
KEYWORDS
EST.
SOURCE
Solanum chacoense (Chaco potato)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 787)
German,H., Rudd,S., Zotti,C., Caron,S., O'Brien,M., Chantha,S.-C.,
Lagace,M., Major,F. and Matton,D.P.
A 6374 unigene set corresponding to low abundance transcripts
expressed following fertilization in Solanum chacoense Bitt., and
expression profile of 30 receptor-like kinases
Unpublished (2005)
Contact: Daniel P. Matton
Daniel P. Matton
Universite de Montreal
Institut de recherche en biologie vegetale, 4101 rue Sherbrooke
est, Montreal, QC, Canada, H1X 2B2
Tel: 5148723967
Fax: 5148729406
Email: dp.matton@umontreal.ca.
FEATURES
Source
1..787
/organism="Solanum chacoense"
/mol_type="mRNA"
/db_xref="taxon:4108"
/tissue_type="2-6 days post-pollination ovaries"
/dev_stage="Zygotic to globular embryo"
/lab_host="SOLR"
/clone_lib="SV6"
/notes="Organ: Deparicarped ovary/ovules with placenta
tissue; Vector: pBS SK; Site 1: EcoRI; Site 2: XhoI;
Deparicarped ovaries were isolated from a compatible cross
between self-incompatible accessions having the S12S14
self-incompatibility alleles (G4 line as female) and
S11S13 self-incompatibility alleles (V22 line as male).
Those two lines were derived from the parental lines PI
458314 (which carries the S11 and S12 self-incompatibility
alleles) and line PI 230582 (which carries the S13 and
S14 alleles) obtained through the Potato Introduction
Station (Sturgeon Bay, WI). Plants were grown in
greenhouses under natural light, fruit collection took
place in the morning during summer (approx. 14h daylight),
and fruits were pooled from different plants. Total RNA
was isolated as described in EMBO J. 4: 2411-2418, 1985.
The poly A+ RNA was purified from the total RNA by
affinity chromatography using oligo dt agarose beads type
VII (Amersham). Mean Clone length of the library was 1,5
kb."
ORIGIN
Query Match 8.1%; Score 116.8; DB 8; Length 787;
Best Local Similarity 65.2%; Pred. No. 5.4e-18;
Matches 172; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
QY 882 TATTCAATGACAAATGACCCAGAAATGTTTGTCAAGTGGCAAAAGGGGAGACCGGGTA 941
Db 265 TGTACAGTGGCAGAGCAATCCGCACATTTACAGGCCTGGCAGGAAGGCAAAACGGGATA 206
QY 942 CCTATAATTGATGCGCGCAATGGGCACTGATCAAACTGGTTGGATGCACAATCGCTT 1001
Db 205 CCGGATTGTTGATGCGCGCTATGCGTCAGCTTAACAGCACTGGCTGGATGCATACAGGCT 146
QY 1002 AGAATGATTACTGCTCTTTTTTACTTAAATAATTACACATCGATTGGCGTTGGGGTGA 1061

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Db 145 ACGGATGATTACAGCCAGTTTTCTGTGAAGAATTTATTGATCGACTGGCGGAGCGGA 86
QY 1062 AAAATACTTTCAAAAAAATGTTGATGTGACTATGATGTGCCAAATAATATCGGTGGCTGCA 1121
Db 85 GCATATTTCATGTCGAGCTGATTGATGTGATTTGGCAGCAATAACGGTGGCTGGCA 26
QY 1122 ATGGGCTGCTTCAACAGGAACGGA 1145
Db 25 GTGGGCGCTTCAACCGGAACCGA 2
RESULT 8
CD458345 740 bp mRNA linear EST 14-JUN-2004
LOCUS
DEFINITION
Fg08 12109_A Fg08 AAFc ECORC Fusarium graminearum complex_substrate
Gibberella zeae cDNA clone Fg08_12109, mRNA sequence.
CD458345
ACCESSION
VERSION
CD458345.1 GI:31373085
KEYWORDS
EST.
SOURCE
Gibberella zeae
ORGANISM
Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 740)
Watson,R.J., Heyes,R., Chapados,J., Couroux,P., Harris,L.J.,
Hattori,J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A.,
Sprott,D. and Tinker,N.A.
A cDNA library prepared from Fusarium graminearum grown on a
complex plant substrate
Unpublished (2003)
Contact: Watson, Robert.J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA
Tel: (613) 759-1655
Fax: (613) 759-1701
Email: watsonrj@agr.gc.ca.
FEATURES
Source
1..740
/organism="Gibberella zeae"
/mol_type="mRNA"
/db_xref="DAOM 180378"
/db_xref="taxon:5518"
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/dev_stage="Asexual"
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ubstrate"
/notes="Vector: pBluescript II+; Site 1: EcoRI; Site 2:
XhoI; Fusarium graminearum grown on a complex plant
substrate-- wheat leaves treated to remove most of the low
molecular weight, water-soluble components."
ORIGIN
Query Match 7.9%; Score 113.2; DB 6; Length 740;
Best Local Similarity 55.3%; Pred. No. 4.2e-17;
Matches 260; Conservative 0; Mismatches 208; Indels 2; Gaps 2;
QY 807 GCGGACTTTTACAAATATGATCTATAGTGGCTTTCCACAAACAAAGAGGAGTATTCA 866
Db 40 GCGAGACTTTTACAAACATGTTCTGTCAACTGGCCATACGTCTGTATGAACAGCCCTTTA 99
QY 867 AG-AAAAATTCGTTTATTTCAATGGCAAAATGACCCAGAAATGTTTGTCAAGTGGCAA 925
Db 100 AGCCGGAATCTCAAAACATATCGTGGTTCATATGATAACGACACCTTTTCACGGTGGTGG 159
QY 926 AAGGGGACGGGTGACCTATATTTGATGCGCAATGCGCAACTGCAACTCAAACTGTTT 985
Db 160 AGGCGCGACAGGTTTCCCAATTTGGACGAGCTATGCGACAGTGAATACGATAGTT 219
QY 986 GGATGCAAAATCGCTTTAAGAAATGATTACTGCTCTTTTTTAGTAAAAAATTTACACATCG 1045

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USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7044
Fax: 713-798-7078
Email: mgrusak@bcm.tmc.edu
B398204e
TIGR sequence name: MTPAS54TK
More information is available at: www.medicago.org
Seq primer: SKmod (CTA GAA CTA Gtg gat CC).

FEATURES

Location/Qualifiers
1..748
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="Al7"
/db_xref="taxon:3880"
/clone="PGESD10J11"
/tissue_type="immature seeds"
/dev_stage="Immature seeds, 11 to 19 days after pollination"
/clone_lib="GSD"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Immature seeds, collected from pods ranging in age from 11 to 19 days after pollination, were harvested from greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."

ORIGIN

Query Match 7.3%; Score 104.6; DB 3; Length 748;
Best Local Similarity 50.9%; Pred. No. 5.9e-15;
Matches 248; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

QY 882 TATTCATGACAAATGACCCAGAAATGTTTCTCAAGTGGCAAAAGGGGAGACGGGTA 941
DB 1 TTTTCTTGGAAATACCGATCTCTCAAGTTAAGGCTTGAGGCTAGGTAGGCTGGATA 60

QY 942 CCTATAATGTATGCGCAATGCGACAACTGAATCAAACTGTTGATGACCAATCGCTT 1001
DB 61 TCCATTAGTTGATGCAAGGATGAGGAGCTTTGGGCGACCGATGGATACACAACAAAAT 120

QY 1002 AAGATGATGATGCTCTCTTTTGTAGTTAAATTTACACATGATGCGGTTGGGTGA 1061
DB 121 GCGAGTTATAGTTTCTAGTTTTCAGTGAAATGTTGCTTATACCATGGAATGGGAAT 180

QY 1062 AAAATCTTTCAAAAATGTTGATTCAGTATGATGCTGCAATATATCGGTGGCTGGCA 1121
DB 181 GAAATATTTTGGGATACACTATTAGTGTGACCTTGAAGTATATCTTGGTTGGCA 240

QY 1122 ATGGGCTGCTTCAACAGGAACGACGCTGTCCCTTATTTTCGATTTTTATCCAAATAT 1181
DB 241 GTATATCTCGGGAGCTTACCTGATGTCACGAGCTTGAGCGTTAGACGATCCAGAGAT 300

QY 1182 CCAGTCAAAAATTTGTAATGACCGCGATTTTCATCAAAAATATGTTCCAGAACTTAA 1241
DB 301 TCAAGGACGAAATACGATCCAGAGCGGAATACATTCGACATGCTTACCGAGTTGCG 360

QY 1242 GCAAGTCCCAAAAGTATATTCATCAACCAATCTAATGAACGAAGCCTTACAAACGCA 1301
DB 361 AAGAAATTCCAACTGAGTGGATCCATCATCTCGAATGCCACCTACTGTGCTAAAGC 420

QY 1302 ATATCATGTATACATTTAGGAGAAATATCAAAACCCATTTGTGATTTATGATCAAGTAA 1361
DB 421 ATCAGGTATAGATTAGTCAAAACTATCCAAACCAATCATTTGAAATAGATTGCTAG 480

QY 1362 AAAACAA 1368

Db 481 AGAACAA 487

RESULT 15

BQ854812

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Lactuca sativa

Lactuca sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; campanulids; Asterales; Asteraceae; Cichorioideae;

Cichorioideae; Lactuca.

1 (bases 1 to 699)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,

Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,

Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,

Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project

http://compenomics.ucdavis.edu/

Unpublished (2002)

Contact: Alexander Kozik [R.W.Michelmore]

Department of Vegetable Crops, R.W.Michelmore Lab

University of California at Davis (UCD)

Asmudson Hall, UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]

singleton, see http://cgdb.ucdavis.edu/ for details.

Plate: QGB24 row: E column: 15.

Location/Qualifiers

1..699

/organism="Lactuca sativa"

/mol_type="mRNA"

/cultivar="Salinas"

/db_xref="taxon:4236"

/clone="QGB24E15"

/lab_host="E.coli"

/clone_lib="QG ABCDI lettuce salinas"

/note="Vector: pBRCDNA5fAB; The library was constructed

from 10 different sources of RNA from a single genotype.

Separate cDNAs were generated using primers that

incorporated unique 5' and 3' tags to distinguish each

source of RNA. cDNAs were then pooled, size-fractionated,

directionally cloned into a custom medium-copy vector and

transformations made with four size classes to minimize

size bias. Details of each source of RNA and library

construction can be obtained at http://cgdb.ucdavis.edu/

TAG_TISSUE=leaves dark grow

TAG_LIB=QG ABCDI lettuce salinas

TAG_SEQ=GCTAGTCGGG"

ORIGIN

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Best Local Similarity 50.8%; Pred. No. 1e-14;
Matches 247; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

QY 787 TTCAAAAGAGATTAGCTTGGCGGACCTTTTCAATATATCATCTATAGTGGTTCCACAA 846
DB 90 TTCTTAAATCAATTGGTTTTCGAAATATTCGCTTACATTTGTTTAAATTTCCATTC 149

QY 847 CAAAAGAGAGAGCTATTCAAGAAAAATTCGTTTATTTCAATGGCAAAATGACCAGAA 906
DB 150 ACTCAGAAAGATCGCTTTTAAAAACTTAAAGTATTTCCCATGGCAAGCTAATGAAGCA 209

QY 907 ATGTTTGTCAAGTGGCAAAAGAGGAGAGGGGTACCCCTATTAATTAATGATCCGCAATGCCA 966
DB 210 CACTTTAAGGCTTGGAGACAGGGTCCGACAGGGTACCCGTTAGTTGATCGGGTATGAGA 269

Qy	967	CAACTGAATCAAACTGGTTGGATCGACAAATCGCTTAAGAATGATTACTGCCTCTTTTTTTA	1026
Db	270	GAGCTTTGGGCAACGGGTTGGCTTCATAATAAGATTCCGGGTGATTACTGCAAGTTTTTTG	329
Qy	1027	GTTAAAAATTTACACATCGATTGGCGTTGGGGTGAAAAATACTTTCAAAAAAATGTTGATT	1086
Db	330	GTCAGTGTGTTTGTGTTGCCCTTGGCAATGGGGGATGAAGTATTTTTTGGGATACGCTTTTG	389
Qy	1087	GACTATGATGTCGCAATAATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGAACGGAC	1146
Db	390	GATCGGATCTTGAAGATGATGTTCTTGGTTGGCAGTATATATCTGGGAGCTTGCCAGAT	449
Qy	1147	GCTGTCCCTTATTTTCGGATTTTTTAATCCAATTTCCAGTCAAAAAAATTTGATAATGAC	1206
Db	450	GGGATGACCTTCGGCGCTTTGATAGCCCCGAGGTTCAAGGATTCAAATATGACCCCGAG	509
Qy	1207	GGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCCACAAAAAGTATATTCAT	1266
Db	510	GGTGAATACATAAGACATGGCTACCCGAAATTATCAAGATACCAACCGATGGATCCAT	569
Qy	1267	CAACCA	1272
Db	570	CATCCA	575

Search completed: December 20, 2005, 21:48:57
Job time : 6270 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using aw model

Run on: December 20, 2005, 16:59:36 ; Search time 296 Seconds
(without alignment)
8611.566 Million cell updates/sec

Title: US-10-758-979-2
Perfect score: 1434
Sequence: 1 atgaagagagtaatatggtt.....acaatccaaaggttccaataa 1434

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
5: /cgn2_6/prodata/1/ina/H COMB.seq.*
6: /cgn2_6/prodata/1/ina/pCTUS COMB.seq.*
7: /cgn2_6/prodata/1/ina/pp COMB.seq.*
8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	942	65.7	966	US-09-134-000C-1312	Sequence 1312, Ap
2	597	41.6	609	US-09-134-000C-1313	Sequence 1313, Ap
3	212.2	14.8	1446	US-09-543-681A-4149	Sequence 4149, Ap
4	206.2	14.4	1393	US-08-956-171B-594	Sequence 594, App
5	206.2	14.4	1393	US-08-781-986A-594	Sequence 594, App
6	203.4	14.2	1608	US-09-328-352-389	Sequence 389, App
7	201.4	14.0	5024	US-08-920-812-7	Sequence 7, Appli
8	201.4	14.0	5024	US-08-920-812-7	Sequence 7, Appli
9	201.4	14.0	5024	US-08-921-177-7	Sequence 7, Appli
10	201.4	14.0	5024	US-08-362-577C-7	Sequence 7, Appli
11	201.4	14.0	5024	US-08-920-828-7	Sequence 7, Appli
12	199	13.9	1380	US-09-134-001C-2629	Sequence 2629, Ap
13	184.8	12.9	640681	US-09-790-988-1	Sequence 1, Appli
14	137.2	9.6	1698	US-09-614-221A-226	Sequence 226, App
15	117.4	8.2	1248	US-09-489-039A-6144	Sequence 6144, App
16	109.8	7.7	1638	US-09-252-991A-13995	Sequence 13995, A
17	109.8	7.7	2514	US-09-252-991A-14142	Sequence 14142, A
18	102.6	7.2	2200	US-08-272-255-21	Sequence 21, Appl
19	102.6	7.2	2200	PCT-US95-08565-21	Sequence 21, Appl
20	80	5.6	2458	US-08-272-255-5	Sequence 5, Appli
21	80	5.6	2458	PCT-US95-08565-5	Sequence 5, Appli
22	74	5.2	1977	US-08-272-255-17	Sequence 17, Appl
23	74	5.2	1977	PCT-US95-08565-17	Sequence 17, Appl
24	62.4	4.4	330	US-09-489-039A-5657	Sequence 5657, Ap

25	48.2	3.4	1141	3	US-09-806-708B-22	Sequence 22, Appl
26	47.2	3.3	1664976	3	US-08-916-421B-1	Sequence 1, Appli
27	47.2	3.3	1664976	3	US-09-692-570-1	Sequence 1, Appli
28	43.2	3.0	832	3	US-09-621-976-2813	Sequence 2813, Ap
29	42.4	3.0	1241	2	US-07-593-657-6	Sequence 6, Appli
30	42.4	3.0	1241	3	US-08-942-012B-3	Sequence 3, Appli
31	41.8	2.9	1141	3	US-09-806-708B-22	Sequence 22, Appli
32	40.6	2.8	492	3	US-09-270-767-6893	Sequence 6893, Ap
33	40.6	2.8	492	3	US-09-270-767-22175	Sequence 22175, A
34	40.6	2.8	601	3	US-09-949-016-185665	Sequence 185665,
35	40.6	2.8	113966	3	US-09-949-016-12277	Sequence 12277, A
36	40.6	2.8	113967	3	US-09-949-016-17051	Sequence 17051, A
37	40.2	2.8	1710	3	US-09-618-425-6	Sequence 6, Appli
38	40.2	2.8	2450	3	US-09-618-425-4	Sequence 37, Appli
39	40.2	2.8	3976	3	US-09-244-805-37	Sequence 4378, Ap
40	40	2.8	1680	3	US-09-248-796A-4378	Sequence 6612, Ap
41	39.6	2.8	349	3	US-09-270-767-6612	Sequence 21894, A
42	39.6	2.8	349	3	US-09-270-767-21894	Sequence 5237, Ap
43	38.8	2.7	1782	3	US-09-248-796A-5237	Sequence 17195, A
44	38.8	2.7	129658	3	US-09-949-016-17195	Sequence 166954,
45	38.6	2.7	601	3	US-09-949-016-166954	

ALIGNMENTS

RESULT 1
US-09-134-000C-1312
; Sequence 1312, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1312
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1312

Query Match	65.7%	Score 942;	DB 3;	Length 966;
Best Local Similarity	99.9%	Pred. No. 2.3e-252;		
Matches 953;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;
QY	1	ATGAAAAGAGTAATATGTTTACAGCTGATTTACGATTACAGGATAATAAGCATTAGCA	60	
Db	13	ATGAAAAGAGTAATATGTTTACAGCTGATTTACGATTACAGGATAATAAGCATTAGCA	72	
QY	61	CACGGTTTACAAAATCTGCACCTCATGAATGATTTTATTATTCCTCAATCTCTCAA	120	
Db	73	CACGGTTTACAAAATCTGCACCTCATGAATGATTTTATTATTCCTCAATCTCTCAA	132	
QY	121	CAATTTATTCAGAAAGTGCTAATCATACGCTTTTTCGAGCTTAGCTCGTTTCAAA	180	
Db	133	CAATTTATTCAGAAAGTGCTAATCATACGCTTTTTCGAGCTTAGCTCGTTTCAAA	192	
QY	181	GAACGAATGCATCAAGAGCATTACAAATCATGCTGGCGGACCATTTAGATTATTT	240	
Db	193	GAACGAATGCATCAAGAGCATTACAAATCATGCTGGCGGACCATTTAGATTATTT	252	
QY	241	TCACGTTTGAACGCAAAATACCGATTGGCAGGCATTATTTTAAATGAAGATCTGT	300	
Db	253	TCACGTTTGAACGCAAAATACCGATTGGCAGGCATTATTTTAAATGAAGATCTGT	312	
QY	301	GGCTTTGGGCGCAAGCGGACCAAGCTATCGCTTTTGTGAAGAAAATATATTCAG	360	

Db 313 GGCTTTGGGCAAGCGGACAGCAAGCTATGCGCTTTTGAAGAAAATAATATTCAG 372
Qy 361 TCTTTCCTTTCAAGATGCTTATTTGATGGCTCTGAAGAAATTAAGAAGACGATGGC 420
Db 373 TCTTTCCTTTCAAGATGCTTATTTGATGGCTCTGAAGAAATTAAGAAGACGATGGC 432
Qy 421 AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAATGGAAGAGCGCCTAAAGAAACA 480
Db 433 AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAATGGAAGAGCGCCTAAAGAAACA 492
Qy 481 CCGATTCTGTTTCTCTATACAGCTGAAGAAAATTTTAGTGGCTGTCTTTTCCAGAAGAG 540
Db 493 CCGATTCTGTTTCTCTATACAGCTGAAGAAAATTTTAGTGGCTGTCTTTTCCAGAAGAG 552
Qy 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTTAACACACTATAGTGTGGCGAA 600
Db 553 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTTAACACACTATAGTGTGGCGAA 612
Qy 601 GAAACAGCCAGAGCGCTTAAATACCTTTTATGATCAAAACCTTCAATCCTATGAAAT 660
Db 613 GAAACAGCCAGAGCGCTTAAATACCTTTTATGATCAAAACCTTCAATCCTATGAAAT 672
Qy 661 AAGCGTGATTTTCTTATCAGGATCAACAGAGTCACTGTCTACTTTTTTAAGAACGGGA 720
Db 673 AAGCGTGATTTTCTTATCAGGATCAACAGAGTCACTGTCTACTTTTTTAAGAACGGGA 732
Qy 721 GAACCTTCGATTCGACCAATTTGGAGAGCTTGGATCTGTGCTCTCTAGCTTAAGTAAA 780
Db 733 GAACCTTCGATTCGACCAATTTGGAGAGCTTGGATCTGTGCTCTCTAGCTTAAGTAAA 792
Qy 781 GAAACCTTCAAAAAGAGTACCTTGGCGGACCTTTTACAAATATGATCTATAGTGGCTTT 840
Db 793 GAAACCTTCAAAAAGAGTACCTTGGCGGACCTTTTACAAATATGATCTATAGTGGCTTT 852
Qy 841 CCACAAACAAAGAGGAGCTATTCAAGAAAATTTTCGTATATTCAATGACAAATGAC 900
Db 853 CCACAAACAAAGAGGAGCTATTCAAGAAAATTTTCGTATATTCAATGACAAATGAC 912
Qy 901 CCAGAAATGTTTCAAGTGCGCAAAAGGGGAGAC-GGGGTACCTTAATTGA 953
Db 913 CCAGAAATGTTTGTCAAGTGCGCAAAAGGGGAGACGGGGGTACCTTAATTGA 966

RESULT 2

US-09-134-000C-1313
; Sequence 1313, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1313
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1313

Query Match 41.6%; Score 597; DB 3; Length 609;
Best Local Similarity 99.8%; Pred. No. 2.6e-156;
Matches 608; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 827 TCTATAGTGGCTTTCCACAAACAAAGAGGAGCTATTCAAGAAAATTTTCGTATATTC 886
Db 1 TCTATAGTGGCTTTCCACAAACAAAGAGGAGCTATTCAAGAAAATTTTCGTATATTC 60
Qy 887 AATGACAAATGACCCAGAAATGTTTGTCAAGTGGCAAAAGGGGAGAC-GGGGTACCT 945

Db 61 AATGGCAAAATGATCCAGAAATGTTTGTCAAGTGGCAAAAGGGGAGACGGGGTACCT 120
Qy 946 ATAATTGATCGCGCAATGCGACAACCTGAATCAAACTGGTGGATGCACAATCGCTTAA 1005
Db 121 ATAATTGATCGCGCAATGCGACAACCTGAATCAAACTGGTGGATGCACAATCGCTTAA 180
Qy 1006 ATGATTACTCGCTCTTTTGTAGTTAAAAATTTACACATCGATTGGCGGTGGGGTGA 1065
Db 181 ATGATTACTCGCTCTTTTGTAGTTAAAAATTTACACATCGATTGGCGGTGGGGTGA 240
Qy 1066 TACTTTCAAAAAATGTTGATTGACTATGCTGCCAAATAATATCGTGGCTGGCAATGG 1125
Db 241 TACTTTCAAAAAATGTTGATTGACTATGCTGCCAAATAATATCGTGGCTGGCAATGG 300
Qy 1126 GTGTCTTCAACAGAACGCGCTGCTCTTATTTTCGGATTTTAAATCAAAATATCCAG 1185
Db 301 GCTGTCTTCAACAGAACGCGCTGCTCTTATTTTCGGATTTTAAATCAAAATATCCAG 360
Qy 1186 TCAAAAAATTTGATATGACGCGCTTCCATCAAAAAATATGTTCCAGAACTTAAACAA 1245
Db 361 TCAAAAAATTTGATATGACGCGCTTCCATCAAAAAATATGTTCCAGAACTTAAACAA 420
Qy 1246 GTGCCACAAAAGTATATTCATCAACCAAAATCTAATGAACGAAGCTTTACAAACGA 1305
Db 421 GTGCCACAAAAGTATATTCATCAACCAAAATCTAATGAACGAAGCTTTACAAACGA 480
Qy 1306 CATGTACATTTAGAGAAAATTTTCAAAAACCCATTTGTCGATTATGATCAAGTAA 1365
Db 481 CATGTACATTTAGAGAAAATTTTCAAAAACCCATTTGTCGATTATGATCAAGTAA 540
Qy 1366 CAAACATTTGTTCTATATGAAGCGCAAGAAATTCATCAAGAAATGAACAATCCAA 1425
Db 541 CAAACATTTGTTCTATATGAAGCGCAAGAAATTCATCAAGAAATGAACAATCCAA 600
Qy 1426 TTTCAATAA 1434
Db 601 TTTCAATAA 609

RESULT 3

US-09-543-681A-4149
; Sequence 4149, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4149
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-4149

Query Match 14.8%; Score 212.2; DB 3; Length 1446;
Best Local Similarity 60.0%; Pred. No. 6.9e-49;
Matches 418; Conservative 0; Mismatches 258; Indels 21; Gaps 3;

Qy 596 GCGAAGAACACGCGGCTTAAATACTTTTATGTATCAAAAACTTCAATCTCATG 655
Db 635 GCGAAGAACACGCGGCTTAAATACTTTTATGTATCAAAAACTTCAATCTCATG 694
Qy 656 AAATAAGCGTGTATTTCTTATCAGGATCAACAGGATCATCTCTACTCTTTTAA 715
Db 695 CAAAATGGCGAGATATTCCTGCTATTGATGGAACCAAGTCAATATCCCTTATCT 754
Qy 716 CGGAGAACTTTCGATTGCAACCATTTGGCAAGAGCTTGC---ATCTGTGCTTCTAGCT 772

FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 594:
SEQUENCE CHARACTERISTICS:
LENGTH: 1393 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 594:
US-08-956-171E-594

Query Match 14.4%; Score 206.2; DB 3; Length 1393;
Best Local Similarity 56.2%; Pred. No. 3.2e-47;
Matches 432; Conservative 0; Mismatches 328; Indels 9; Gaps 2;

627 TTTTATTGATCAAAAACTTCAATCCCTATGAAATTAAGCGTGAATTTCTTATCAGGATCA 686
617 TTTTATTGATCAAAAACTTCAATCCCTATGAAATTAAGCGTGAATTTCTTATCAGGATCA 676
687 AACGAGTCATCTGTCTACTTTTAAAGAACGGGAGAACTTTTCGATTCGCACTTGGCA 746
677 AACAGTCAGCTAAGTGTCTTTAGCATATGATTTATAGATATTTTACCTGAATTT 736
747 AGA-----GCTTGCACTCTGTGCTTCTAGCTTAAGTAAAGAAACCTTCAAAAAGATTT 800
737 TGATTTTATGCGCGCTTATGATGAAGATGAGGCAAACTATGAAGCATTTTATCGTGAAT 796
801 AGCTTGGCGGACTTTTACAAATATGATCTATAGTGGCTTTCCCAACAAAAAGAGGAGC 860
797 CATTTTATAGAGATTTTATGATGTTTAAATGACACAGTATCTTGAACCTCATACCAAGC 856
861 TATTCAGAAAAATTTTCGTTTATTTCAATGGACAAATGACCCAGAAATGTTTGTCAAGTG 920
857 TTTCAAACTTAATATCGACAGATAAATGTCGCAAAATGAAGCGATTTTATGATGATG 916
921 GCAAAAAAGGAGACGGGGTACCCCTATAATATGATGCGGCAATGCGCACTGAATCAAC 980
917 GTGGAAGGCAACAGGATTTTCAATCATTTGATGACAGCAATATGGAATTTGACACAAAC 976
981 TGGTTGATGACAAATCGCTTAAGAATGATTACTGCTCTTTTGTAGTAAATTTTACA 1040
977 TGGTTTATGCAATTAATCGAATGAGATGTTGTGTCGCAATTTTAAACCAAGATTTAT 1036
1041 CATCGATTGGGCTTGGGGTGAAAAATACTTTCAAAAAATGTTGATTTGACTATGATGTC 1100
1037 TATGATGACATGGGAGAAAAATTTCTTTAGAAAGCACTTTATGATGATGATGATGATG 1096
1101 CAATTAATATCGGTGGCTGGCAATGGCTGCTTCAACAGGAAACGGACGCTGCTTATTT 1160
1097 ATCAATATTCATGATGGCAATGGCTGCTTCTTACAGGTACGGATGCGGTGCTATTT 1156
1161 TCGGATTTTATCCCAATTTATCCAGTCAAAAAATTTGATTAATGACGCGCACTTATCA 1220
1157 TAGAATGTTTAAATCCAAATAGACAGAGTGAACGCTTTGATGCTAAAGCTTTGTATAT 1216
1221 AAAATATGTTCCAGAACTTAAGCAAGTGCACAAAAAGTATATTTTATCAACCAAAATTA 1280
1217 AACATATCTCCGATTTTAAATCAAAATGATGCAAAATATTTGATGATGATGATGATG 1273
1281 GAACGAAGCTTTCAAAACGCAATATCATGTACATTTTAGGAGAAAATTTATCAAAACCC 1340
1274 CAATGAGTCCAACTTTTGAACAGGGGATTTGAATTTAGGTAGTCAATTTATCAAGACA 1333
1341 TGTGATTTGATCAAGTAAAGAAAAACAAACATTTGTTTCTATATGAAGCG 1389
1334 GGTAGATCATCAAGAAAAACGTACACAAAGTTTGTAGCTACATTTTAAAGCG 1382


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Qy 930 GGAGACGGGTACCTTAATTTGATCGCGCAATGCGCAACTGAATCAAACTGTTGGAT 989
Db 1167 TCAACCGGTATCTTATTTGATGCTGGATGCGCAACTTTTACAAACAGCTGGAT 1226
Qy 990 GCACAATCGCTTAAGAATGATCTGCTCTTTTGTAGTTAAATTTACACATCGATTG 1049
Db 1227 GCATAATCGAGTACGTATGATTTACAGCCATGTTTTTATGTAAATACTTTTGTATTG 1286
Qy 1050 GCGTGGGGTGAATAATCTTTCAAAAAATCTTGATTGACTATGATGCTGCCAATAATAT 1109
Db 1287 GCGCATTTGGTGAACAATGGTTTATGCGACATTTAATGATGGTACCTCGCGCAATAA 1346
Qy 1110 CGGTGGCTGGCAATGGCTGCTTCAACAGGAACGAGCGCTGCTCCCTTATTTTCGATTTT 1169
Db 1347 TGGCGGTTGGCAATGGTGTGCTCAACAGGAACAGATGCGGTACCTTATTTTCGATTTT 1406
Qy 1170 TAATCCAATTTCCAGTCAAAAAAATTTGATAATGACGGCCAGTTTCATCAAAAAATATGT 1229
Db 1407 CAACCAATTTGCTCAATCAAGAAGTTTGTATCCGGAGGAGAAATATATTCGCCAATGGGT 1466
Qy 1230 TCCAGAACTTAAGCAAGTCCCAAAAGTATATTCATCAACCAATCTAATGAACGAAGC 1289
Db 1467 GAAAGATTTGGCTCAATTTGGCAATTAACCAATTCATGAACCTTACTCAAGCAAAACCGA 1526
Qy 1290 CTTCAAAACGCAATATCATGTACATTTTAGGAGAAAAATTTATCAAAACCCATTTGCGATTA 1349
Db 1527 TCTTGGTTTAATTTCAAAACCCATAGTAATTTAAAGAAACACGCTTAAAGCAAT 1586
Qy 1350 TGCATCAAGTAAAAA 1364
Db 1587 TGAACCTTCAAGAA 1601
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RESULT 7

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US-08-920-812-7
; Sequence 7, Application US/08920812
; Patent No. 5763188
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,812
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laurea, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 5024 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus epidermidis
; STRAIN: Clinical Isolate SE-32
; US-08-920-812-7
Query Match 14.0%; Score 201.4; DB 2; Length 5024;
Best Local Similarity 58.7%; Pred. No. 1.2e-45;
Matches 368; Conservative 0; Mismatches 256; Indels 3; Gaps 1;
Qy 774 AAGTAAAGAAACCTTCAAAAAAGAAATTTAGCTTGGCGCGACTTTTACAAATATGATCTATAG 833
Db 3624 AAATTACGAAACITTTATACGTGAATTTATTTTAGAGAGTTTATTTATGATTTAATGAC 3683
Qy 834 TGGCTTTTCCACACAAAGAGAGAGCTATTTCAAGAAAAATTTTGGTTATATTCATGAC 893
Db 3684 CAATTATCCGGAACAGCTCATGTGCTTTTAAAGAAAAATACCAACAATTTGAAATGGTC 3743
Qy 894 AATGACCCAGAAATGTTTGTCAAGTGCACAAAAAGGGAGACGGGTACCCCTATAATTGA 953
Db 3744 TTATAATGAAGAGAAATTTTAACTGTGGAAGATGGGAATACTGCTTTTCCAAATTTGA 3803
Qy 954 TGGCGCAATCGCAACACTGAATCAAACTGGTTGGATGCGCAACATCGCTTAAAGAAATGATTC 1013
Db 3804 TGCAGCAATGGAGGAACCTTAAACAACCTGGATTTATGCAATATCGCATGAGATGGTAGT 3863
Qy 1014 TGCCTCTTTTGTAAAAATTTACACATCGATTTGGGCTGGGGTGAATAATCTTTTCA 1073
Db 3864 TTCTCAATTTTAACTAAAGATTTGTTTATTTGACTGGATTTGGGGGTGAGTCAITTTTCAA 3923
Qy 1074 AAAAATGTTGACTATGATGCTGCCAATATATCGTGGCTGGCAATGGGCTGCTTC 1133
Db 3924 ACAAAAATTAATAGATTATGATGCGCTTCAAAATGTTTACGAGATGGCAGTGGTCAGCTTC 3983
Qy 1134 AACAGGAACGACGCTGCTCCCTTATTTTTCGGATTTTAAATCCAAATTTATCCAGTCAAAAA 1193
Db 3984 TACTGGAAACAGATGCTGTACCATCTTTAGAAATGTTTAAATCCCTATTAAGACAAAGCAGCG 4043
Qy 1194 ATTTGATAATGACGGCCAGTTTCATCAAAAAATATGTTTCCAGAACTTTAAGCAAGTGCACA 1253
Db 4044 TTTTGATAATAATGCACGATATATAAAAACTTACATTCCAAGATTTAAATCAGGTAGATGC 4103
Qy 1254 AAAGTATATTCATCAACCAATCTTAATGAACGAGCTTACAAACGCAATATCATGTACA 1313
Db 4104 TAAGTATTTACACGATACTCATAAATTCGAGCAACAAATAAAGGGGCAA---GGTGTGA 4160
Qy 1314 TTTAGGAGAAATTTATCAAAACCCATTTGTCGATTATGTCATCAAGTAAAAAACAAACATT 1373
Db 4161 AATAGGTAAGACTATCTCTAAACAATGATTCACAAAGAAAGTAGACAAACGTTGTAAT 4220
Qy 1374 GTTTCTATATGAACGAGCAAGAAAT 1400
Db 4221 GTCAGAAATTCAAAGCTATAGATTAAT 4247
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RESULT 8

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US-08-920-827-7
; Sequence 7, Application US/08920827
; Patent No. 5770375
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotugu
; APPLICANT: Eda, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
```

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; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/920.827
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5024 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus epidermidis
; STRAIN: Clinical Isolate SE-32
; US-08-920-827-7

Query Match          14.0%; Score 201.4; DB 2; Length 5024;
Best Local Similarity 58.7%; Pred. No. 1.2e-45;
Matches 368; Conservative 0; Mismatches 256; Indels 3; Gaps 1;

QY 774 AAGTAAAGAAACCTTCAAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCTATAG 833
DB 3624 AAATTACGAACTTTTATACGTGAATGATTTTAGAGAGTTTATATGATTAATGAC 3683
QY 834 TGCCTTTCCACAAACAAAGAGAGCTATTCAAGAAAAATTTTCGTTATATTCATGAC 893
DB 3684 CAATTATCCGAAACAGCTCATGTTGCTTTTAAAGAAAAATACCAACAATTGAAATGGTC 3743
QY 894 AAATGACCCAGAAATGTTTGTCAAGTGCACAAAAGGGGAGCGGTACCTATAATTGA 953
DB 3744 TTATAATGAAGAGAAATTTTAAACTGTGGAAGATGGGAATACTGTTTCCAAATATTGA 3803
QY 954 TGCCGAATGCGACAACTGAATCAAACTGGTTGGATGCACAACTCGCTTAAGAAATGATTAC 1013
DB 3804 TGCAGCAATGAGGAACCTTAAACAACTGGATTTATGCAATACGATGAGATGGTAGT 3863
QY 1014 TGCCTCTTTTATGTTAAATTTTACACATCGATTTGGCGTTGGGGTGAATAATCTTCA 1073
DB 3864 TTCTCAATTTTAACTAAAGATTTGTTTATTGACTGGATTTGGGGTGGAGTCAATTTTCAA 3923
QY 1074 AAAATGTTGATTGACTATGATGTCGCAATAATATCGGTGGCTGGCAATGGGCTGCTTC 1133
DB 3924 ACAAAAAATTAATAGATATGATGACGCTTCAAAATGTTTCACGGATGGGAGTGGTCAGCTTC 3983
QY 1134 AACAGGACGACGCTGTCCTTTATTTTCGATTTTAAATCCAATTTTCCAGTCAAAAAA 1193
DB 3984 TACTTGGAACAGATGCTGTACCACTTTAGATGTTTAACTCTTATAGACAAACGAGCG 4043
QY 1194 ATTTGATAATGACGGCCAGTTTCATCAAAAAATATGTTTCCAGAACTTAAGCAAGTGCCACA 1253
DB 4044 TTTTGATAAATATGCACGATATATAAAAACTTACATTTCCAAAGATTTAAATCAGGTAGATGC 4103
QY 1254 AAGTATATTTCATCAACCAAACTTAATGAACGAAGCCCTTACAAACGCAATATCATGTACA 1313
```

```
DB 4104 TAAGTATTTACACGATACCTATAAAATTCGAGCAACAATAAAGGGGCAA---GGTGTGA 4160
QY 1314 TTTAGGAGAAATTTCCAAAACCCATTTGTGATTTATGATCAAGTAAAGAAACAAACATT 1373
DB 4161 AATAGGTAAGAGCTATCTCTAAACAAATGATTGATCAAAAGAAAGTAGACAACGTTGTAAT 4220
QY 1374 GTTCTTATATGAACGCGACCAAGAAAT 1400
DB 4221 GTCAGAAATCAAAAGCTATAGATTAAAT 4247

RESULT 9
US-08-921-177-7
; Sequence 7, Application US/089211177
; Patent No. 5798211
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Matsuhisa, Akio
; APPLICANT: Uehara, Hirotsugu
; APPLICANT: Ega, Soji
; TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/921,177
; FILING DATE: 29-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,577
; FILING DATE: 27-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 19036/32420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5024 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Staphylococcus epidermidis
; STRAIN: Clinical Isolate SE-32
; US-08-921-177-7

Query Match          14.0%; Score 201.4; DB 2; Length 5024;
Best Local Similarity 58.7%; Pred. No. 1.2e-45;
Matches 368; Conservative 0; Mismatches 256; Indels 3; Gaps 1;

QY 774 AAGTAAAGAAACCTTCAAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCTATAG 833
DB 3624 AAATTACGAACTTTTATACGTGAATGATTTTAGAGAGTTTATATGATTAATGAC 3683
QY 834 TGCCTTTCCACAAACAAAGAGAGAGCTATTCAAGAAAAATTTTCGTTATATTCATGAC 893
DB 3684 CAATTATCCGAAACAGCTCATGTTGCTTTTAAAGAAAAATACCAACAATTGAAATGGTC 3743
```


ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
Prior APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5024 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Staphylococcus epidermidis
STRAIN: Clinical Isolate SE-32
US-08-920-828-7

Query Match 14.0%; Score 201.4; DB 2; Length 5024;
Best Local Similarity 58.7%; Pred. No. 1.2e-45;
Matches 368; Conservative 0; Mismatches 256; Indels 3; Gaps 1;

QY 774 AAGTAAGAAACCTTCAAAAAGAGTAGCTTGGCGGACTTTTACATATGATCTATAG 833
DB 3624 AAATTACGAACTTTTATACGTGAATTGATTTTAGAGAGTTTATTATGTAATTAATGAC 3683

QY 834 TGGCTTTCCACAAAGAGGAGCTATTCAAGAAAAATTCGTTATATTCATGGAC 893
DB 3684 CAATTATCCGAACAGCTCATGTTGCTTTTAAAGAAAAATACCAAAATTTGAATGGTC 3743

QY 894 AAATGACCCAGAAATGTTTGTCAAGTGGCAAAAAGGGAGACGGGTACCCCTATAATTGA 953
DB 3744 TTATAATGAAGAGAATTTTAAACTGTGGAAGATGGGAATACTGGTTTCCAAATTAATGA 3803

QY 954 TGGCGCAATGGCAACACTGAATCAACTGTTGATGCAACATCGCTTAGAAGATTAC 1013
DB 3804 TGCAGCAATGAGGAACCTTAAACAACTGGGATTTATGCAATAATCGCATGAATGGTAGT 3863

QY 1014 TGCCTCTTTTGTAGTTAAATTTTACATCATCGATTGGGTTGGGTTGAAAAATCTTTCA 1073
DB 3864 TTCTCAATTTTAACTAAAGATTTGTTTATGACTGGATTGGGTTGAGTCATTTTTCAA 3923

QY 1074 AAAAATGTTGATGATGATGCTGCGCAATTAATATCGTGGCTGGCAATGGGCTGCTTC 1133
DB 3924 ACAAAAATTAATAGATTATGATGACGCTTCAAAATGTTTCAAGGATGGCAGTGGTCAGCTTC 3983

QY 1134 AACAGGACCGACGCTGCTTATTTTCGGATTTTAAATCCATTAATCCAGTCAAAAAA 1193
DB 3984 TACTGGAAACAGATGCTGTACCATACTTTAGAAATGTTTAAATCCTATAAGACAAACGAGCG 4043

QY 1194 ATTTGATAATGACGGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCCACA 1253
DB 4044 TTTTGATTAATGACACGATATAAATACTTACATTCAGATTAATCAGGTAGATGC 4103

QY 1254 AAAGTATATTTCATCAACCAAACTTAATGAACGAAGCCTTCAAAACGCAATATCATGTACA 1313
DB 4104 TAAGTATTACAGGATACATAAATTCAGCAACAAATTAAGGGGCAA---GGTGTGA 4160

QY 1314 TTTAGGAGAAAAATTTATCCAAAACCCCAATTCGTGATTTATGCAATCAAGTAAAAAAACAACATT 1373
DB 4161 AATAGGTAAGAGACTATCTCTAAACAAATGATTGATCACAAGAAAGTAGACAACGTTGTAAT 4220

QY 1374 GTTCTTATATGAGCGAGCAAGAAAT 1400
DB 4221 GTCAGAAATTCAAAAGCTATAGATTAAAT 4247

RESULT 12
US-09-134-001C-2629
; Sequence 2629, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2629
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2629

Query Match 13.9%; Score 199; DB 3; Length 1380;
Best Local Similarity 58.9%; Pred. No. 3.2e-45;
Matches 362; Conservative 0; Mismatches 250; Indels 3; Gaps 1;

QY 774 AAGTAAGAAACCTTCAAAAAGAGTAGCTTGGCGGACTTTTACATATGATCTATAG 833
DB 759 AAATTACGAACTTTTATACGTGAATTGATTTTAGAGAGTTTATTATGTAATTAATGAC 818

QY 834 TGGCTTTCCACAAAGAGGAGCTATTCAAGAAAAATTCGTTATATTCATGGAC 893
DB 819 CAATTATCCGAACAGCTCATGTTGCTTTTAAAGAAAAATACCAAAATTTGAATGGTC 878

QY 894 AAATGACCCAGAAATGTTTGTCAAGTGGCAAAAAGGGAGACGGGTACCCCTATAATTGA 953
DB 879 TTATAATGAAGAGAATTTTAACTGTGGAAGATGGGAATACTGGTTTCCAAATTAATGA 938

QY 954 TGGCGCAATGGCAACACTGAATCAAACTGGTTGGATGCACAATCGCTTAAAGAAATGATTAC 1013
DB 939 TGCAGCAATGGAGGAACTTAAACAACTGGAATTTATGCAATAATCGCATGAGAATGGTAGT 998

QY 1014 TGCCTCTTTTGTAGTTAAATTTTACATCATCGATTGGGTTGGGTTGAAAAATCTTTCA 1073
DB 999 TTCTCAATTTTAACTAAAGATTTGTTTATGACTGGATTTGGGGTGAGTCATTTTTCAA 1058

QY 1074 AAAAATGTTGATGATGATGCTGCAATAATATCGTGGCTGGCAATGGGCTGCTTC 1133
DB 1059 AAAAAATTAATAGATTATGATGACGCTTCAAAATGTTTCAAGGATGGCAGTGGTCAGCTTC 1118

QY 1134 AACAGGACCGACGCTGCTTATTTTCGGATTTTAAATCCAAATTAATCCAGTCAAAAAA 1193
DB 1119 TACTGGAACAGATGCTGTACCATCTTTAGAATGTTTAAATCCTATAAGACAAACGAGCG 1178

QY 1194 ATTTGATAATGACGGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCCACA 1253
DB 1179 TTTTGATAATGACGAGATATATAAAAACTTACATTTCCAAAGATTAAATCAGGTAGATGC 1238

QY 1254 AAAGTATATTTCATCAACCAAACTTAATGAACGAAGCCTTCAAAACGCAATATCATGTACA 1313

Db 1239 TAAGTATTACAGTACTCATAAATTCGACCAACAATAAAGGGCAA---GGTGTGA 1295
 Qy 1314 TTTAGGAGAAATATCCAAACCCATGTCGATTATGTCATCAAGTAAAGAAACAAACATTT 1373
 Db 1296 AATAGTAAAGACTATCCCTAAACAATGATTGATCAACAAGAAAGTAGACACGTGAAT 1355
 Qy 1374 GTTCTTATGAAGC 1388
 Db 1356 GTCAGAAATTCAAAGC 1370

RESULT 13
 US-09-790-988-1
 ; Sequence 1, Application US/09790988
 ; Patent No. 6632935
 ; GENERAL INFORMATION:
 ; APPLICANT: SHIGEMOBU, SHUJI
 ; APPLICANT: WATANABE, HIDEMI
 ; APPLICANT: HATTORI, WASHIIRA
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SIMBIONT OF APHIDS
 ; FILE REFERENCE: 081356/0159
 ; CURRENT APPLICATION NUMBER: US/09/790,988
 ; CURRENT FILING DATE: 2001-02-23
 ; PRIOR APPLICATION NUMBER: JP2000-107160
 ; PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 640681
 ; TYPE: DNA
 ; ORGANISM: Buchnera sp.
 US-09-790-988-1

Query Match 12.9%; Score 184.8; DB 3; Length 640681;
 Best Local Similarity 54.2%; Pred. No. 4.6e-40;
 Matches 465; Conservative 0; Mismatches 357; Indels 36; Gaps 3;

Qy 572 TTCCTTTAACACACTATAGTGTGGCGAAGAAACAGCCGAGAGGGCGCTTAATACATTTTA 631
 Db 331419 TTAATAAATAATTTCTTCTGTTGGAGAAAGAGCGCTATTAAATCGTTTAAATAATTTT 331478
 Qy 632 TTGATCAAAACTTCAATCCTATGAATAAAGCGTATTTTCCTTATCAGGATCAACGA 691
 Db 331479 GTATATATAAATTTAATGATTATTTCTTAAACGAGATTATCCCTTTTGAATGCTACTA 331538
 Qy 692 GTCATCTGTCTACTTTTTTAAGAACGGGAGAACTTTCCGATTCGCACCAATTTGGCAAGAGC 751
 Db 331539 GTATGCTGTCTCCTATATTTATCAGGAGAAATATATCATCTCGATATTTGCTTAAAGTGC 331598
 Qy 752 TTG-----CATCTGTGCTTCTAGCTTAAGTAAAGAAACCTTCAAAAAGAA 798
 Db 331599 TTTTAAACAAACAAACAGCTTCCATTAAATGTTCTTCTAGCTCTCTGTTGTTGATC 331658
 Qy 799 TTAGCTTGGCGGACTTTTACAAATATGATCTATAGTCGTTTCCCAACAAACAAAGAGAA 858
 Db 331659 AGATATTATGGCGTGAATTTTATACCATTTAATTAATGATTTTCCAAATAATTTAGTAGAT 331718
 Qy 859 GCTATTCAAGAAATAATTCG-----TTATATTCAATGGCAAAATGACCCAGAAATGTTTG 913
 Db 331719 CTGAATCATTTAGTAAATCGGAAAGAAATTCATTTGGATTAATAATATAAACAATTTTA 331778
 Qy 914 TCAAGTGGCAAAAGGGGAGACGGGTACCTATAATTTGATGCCGAATGCGCAACTGA 973
 Db 331779 ATGCTTGGAAAGAGAAATACAGGTTTTCCTATAATAGATGCGAGAAATGAGACAATTA 331838
 Qy 974 ATCAAACTGGTGGATGCAATCGCTTAAAGATGATTACTGCTCTCTTTTGTAGTTAA 1033
 Db 331839 ACAGAACTAGGATGGATGCAATTAAGATGATTACATCTAGTTTGTAGTAA 331898
 Qy 1034 ATTTACACATCGATTGGCGTGGGGTGAAATAATCTTTTCAAAAATAATGTTGATTGACTATG 1093

Db 331899 ATCTTTTGATTAATTTGGCGAAGGGAGGAAACATTTTATATCTAATTTTATCGATGGAG 331958
 Qy 1094 ATGCTGCAATAATATCGTGGCTGGCAATGGGCTGCTTCAACAGGAAACGGAGCGCTGTCC 1153
 Db 331959 ACTTAGCGCTGATTAATGGAGGATGGCAATGGTCAAGTGGGATGTTGATTTCTGTAC 332018
 Qy 1154 CTTATTTTCCGATTTTAAATCCAAATATCCAGTCAAAAAAATTTGATAATGAGGCCAGT 1213
 Db 332019 CTTATATAAGAAATTTTAAATCCATCATCAATCAAAAACTTTTGTAGTAATCGGTTAAT 332078
 Qy 1214 TCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCACAAAAAGTATATTCATCAACCAA 1273
 Db 332079 TTATAAAGAAAGTTTATACCAAGATTTAAAAACGTCCTATCATCATATCCATCAACCA 332138
 Qy 1274 ATCTAATGAACGAAGCCTTTACAAACGCAATATATGTCATATTTAGGAGAAATTTATCAA 1333
 Db 332139 AT-----GAATGGTCAAAACAAAAAATTTTAAAAATAGATTATCTTA 332180
 Qy 1334 AACCATTTGCGATTATGTCATCAAGTAAAAACAAAAACAAACATTTGTTCTATATGAAGCGGACA 1393
 Db 332181 ATCCTATTATTAATTTAGTGAAGAGCAAAAAACATCTTTATCGCTATTTCAACAAGCTC 332240
 Qy 1394 AAGAAATTCATCAAGAA 1411
 Db 332241 GATTAAAACTTCATAAAA 332258

RESULT 14
 US-09-614-221A-226
 ; Sequence 226, Application US/09614221A
 ; Patent No. 6723837
 ; GENERAL INFORMATION:
 ; APPLICANT: Karunanandaa, Balasulojini
 ; APPLICANT: Yu, Jaehyuk
 ; APPLICANT: Kishore, Ganesh M.
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
 ; FILE REFERENCE: 16516.075
 ; CURRENT APPLICATION NUMBER: US/09/614,221A
 ; CURRENT FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/142,981
 ; PRIOR FILING DATE: 1999-07-12
 ; NUMBER OF SEQ ID NOS: 626
 ; SEQ ID NO 226
 ; LENGTH: 1698
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces cerevisiae
 US-09-614-221A-226

Query Match 9.6%; Score 137.2; DB 3; Length 1698;
 Best Local Similarity 57.6%; Pred. No. 6e-28;
 Matches 266; Conservative 0; Mismatches 193; Indels 3; Gaps 1;

Qy 782 AAACCTTCAAAAAAGAAATAGCTTGGCGCGACTTTTACA---ATATGATCTATAGTGGCT 838
 Db 1136 AAAATTTTCATCAAGAAGTTGTCATGGAGAGATTTTACAGACATTTGTATGCAACTGGC 1195
 Qy 839 TTCCACAACAAAGAGAGAGCTATTCAGAAAAAATTTTCGTTATATTCATTCGACAAATG 898
 Db 1196 CATATACCTCAATGGGAATGCTTATCGATTGGACACTTTAGATATAAATGGGAGATA 1255
 Qy 899 ACCCAGAAATGTTTCTCAAGTGGCAAAAAAGGGGAGACGGGTACCTTATAATTTGATGCGC 958
 Db 1256 ACCCTGTAGCATTTGAAAAGTGGTACTGTTGTAATACAGGCAATTCCTCATAGTCGATGCA 1315
 Qy 959 CAATCGCAACTGAATCAAACTGGTGGATGCAACAACTGCTTAAGAAATGATTACTGCT 1018
 Db 1316 TAATGAGAAAAATTTACTGTACACAGGCTATATTAATAACAGATCTAGAAATGATCACAGCT 1375
 Qy 1019 CTTTATTTAGTTAAAAATTTTACACATCGATTGGCGTTGGGGTGAAAAATACTTTTCAAAAA 1078
 Db 1376 CTTTCTTTCTAAAAAACCTTTAATAGATTGGAGATGGGGGAGCGCTGTTTATGAAAC 1435

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Qy 1079 TGTGATTGACTATGATCGTCCAATAATATCGGTGGTGGCAATGGGCTGCTTCAACAG 1138
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1436 ACTTGATAGACGGTGATTCGTCCTCAAAATGTTGGTGGCTGGGGTTTTTGTCTAGTACAG 1495
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Qy 1139 GAACGGACGCTGTCCCTTATTTTCGGATTTTAAATCCAATTATCCAGTCAAAAAAATTTG 1198
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1496 GAATTGATGCCCAACCATATTTTAGAGTTTTTTAATATGGATATACAAGCAAAAAAATATG 1555
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Qy 1199 ATAATGACGGCCAGTTTCATCAAAAAAATATGTTCCAGAACTTA 1240
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1556 ACCACAAATGATATTCGTCAACAATGGGTTCCCGAATTGA 1597
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||

RESULT 15
US-09-489-039A-6144
; Sequence 6144, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6144
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6144

Query Match      8.2%; Score 117.4; DB 3; Length 1248;
Best Local Similarity 63.8%; Pred. No. 1.7e-22;
Matches 178; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 919 TGGCAAAAGGGGAGACGGGTACCTATATTTGATCGCGCAATGCGACAACCTGAATCAA 978
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 967 TGGCAGCGCGGGGAGACGGGTTTCCGATTTGATGCCGCCATGCGCCAGCTTAACGCC 1026
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 979 ACTGTTGGATGCACAATCGCTTAAGAATGATTACTGCCTCTTTTGTAGTTAAAAATTTA 1038
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1027 ACCGGCTGGATGCATACCGGTTACGCGATGTTGTCGCCAGCTTCCTGACCAAGATTG 1086
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1039 CACATCGATTGGCGTTGGGGTGAAAAATACCTTCAAAAAAATGTTGATTGACTATGATGCT 1098
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1087 CGCCTCGACTGGCGGGCGGCGAGCGCTATTTCATGAGCCAGCTGATTGATGGCGACCTG 1146
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1099 GCCAATAATATCGGTGGCTGGCAATGGCTTCAACAGGAACGGACGCTGTCCCTTAT 1158
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1147 GCGCGAATAACGCGGCTGGCAGTGGCGGCTTCAACGGGACCCGACCGCGCCCTAT 1206
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1159 TTTCGGATTTTAAATCCAAATTATCCAGTCAAAAAAATTT 1197
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1207 TTCGCATATTTAAACCCACCCACCCAGGGGGAAGTT 1245
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Search completed: December 20, 2005, 20:04:23
Job time : 299 secs

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OM nucleic - nucleic search, using sw model

Run on: December 20, 2005, 17:38:08 : Search time 1284 Seconds
(without alignments)
9235.427 Million cell updates/sec

Title: US-10-758-979-2
Perfect score: 1434
Sequence: 1 atgaagagagaatattggtt.....acaatccaaggtttccaataa 1434

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1434	100.0	1434	US-10-758-979-2	Sequence 2, Appli
2	1434	100.0	2267	US-10-758-979-1	Sequence 1, Appli
3	1432.8	99.9	5277	US-09-070-927A-262	Sequence 262, App
4	526.4	36.7	2460	US-10-398-221-3604	Sequence 3604, Ap
5	518.4	36.2	1163020	US-10-398-221-10	Sequence 10, Appl
6	518.4	36.2	3011208	US-10-398-221-2058	Sequence 2058, Ap
7	416.8	29.1	1451	US-10-398-221-1690	Sequence 1690, Ap
8	206.2	14.4	1393	US-08-781-986A-594	Sequence 594, App
9	206.2	14.4	1393	US-10-329-624-594	Sequence 594, App
10	199	13.9	1380	US-10-724-972A-3359	Sequence 3359, Ap
11	184.8	12.9	640881	US-09-790-988-1	Sequence 1, Appli
12	137.2	9.6	1698	US-10-793-639-226	Sequence 226, App
13	114.8	8.0	1404	US-09-738-626-701	Sequence 701, Appli
14	114.8	8.0	3309400	US-09-738-626-1	Sequence 1, Appli
15	104.2	7.3	1839	US-09-938-842A-479	Sequence 479, App
16	104.2	7.3	1839	US-09-938-842A-479	Sequence 479, App
17	100.4	7.0	3184	US-10-424-599-113803	Sequence 113803, App
18	99.2	6.9	1883	US-10-425-114-5586	Sequence 5586, Ap
19	99.2	6.9	2264	US-10-425-114-19130	Sequence 19130, A
20	99.2	6.9	2533	US-10-425-114-35600	Sequence 35600, A
21	99.2	6.9	2533	US-10-425-115-104197	Sequence 104197, A
22	99.2	6.9	2649	US-10-425-114-24312	Sequence 24312, A
23	99.2	6.9	2721	US-10-425-115-104199	Sequence 104199, A

Sequence 6341, Ap
Sequence 365, App
Sequence 182, App
Sequence 23734, A
Sequence 22489, A
Sequence 30074, A
Sequence 1201, Ap
Sequence 1, Appli
Sequence 1306, Ap
Sequence 124948, A
Sequence 28413, A
Sequence 52170, A
Sequence 14400, A
Sequence 6319, Ap
Sequence 23273, A
Sequence 2479, Ap
Sequence 132131, A
Sequence 52169, A
Sequence 425, App
Sequence 23806, A
Sequence 5999, Ap
Sequence 17600, A

ALIGNMENTS

RESULT 1
US-10-758-979-2
; Sequence 2, Application US/10758979
; Publication No. US20040214208A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Fredrick M.
; APPLICANT: Garsin, Danielle
; APPLICANT: Mylonakis, Eleftherios
; APPLICANT: Calderwood, Stephen B.
; APPLICANT: Sifri, Costi
; TITLE OF INVENTION: Enterococcal Virulence Factors
; FILE REFERENCE: 00786/408002
; CURRENT APPLICATION NUMBER: US/10758,979
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/22979
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,212
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1434
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-758-979-2

Query Match 100.0%; Score 1434; DB 8; Length 1434;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAAGAGTAATATGCTTTAGAGCTGATTTACGATTACAGGATAATAAGCATTAGCA 60
DB 1 ATGAAAGAGTAATATGCTTTAGAGCTGATTTACGATTACAGGATAATAAGCATTAGCA 60
QY 61 CACGGTTTACAAAATTCGACGCTGATGAATGATTTTATTATTCCTCAATGAATCCTCAA 120
DB 61 CACGGTTTACAAAATTCGACGCTGATGAATGATTTTATTATTCCTCAATGAATCCTCAA 120
QY 121 CAATTTATTCAGAAAGTGCTAATCATTAACGCTTTTTTTTTCGAGCTTAGCTCGTTCAA 180
DB 121 CAATTTATTCAGAAAGTGCTAATCATTAACGCTTTTTTTTTCGAGCTTAGCTCGTTCAA 180
QY 181 GAACGATTCGATCAGAGGACATTTACAAATCATGTCGGCGAACCACTTAGATTATTT 240
DB 181 GAACGATTCGATCAGAGGACATTTACAAATCATGTCGGCGAACCACTTAGATTATTT 240

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Qy 241 TCAGTTTGAACGCAAAATTACCCGATTGGCAGGCCAATTTATTTTAATGAAGACTTGT 300
Db 241 TCAGTTTGAACGCAAAATTACCCGATTGGCAGGCCAATTTATTTTAATGAAGACTTGT 300
Qy 301 GGCCTTTGGGCAAGCGGACAGCAAGCTATGCGCTTTTGAAGAAAAATAATTTTCAAG 360
Db 301 GGCCTTTGGGCAAGCGGACAGCAAGCTATGCGCTTTTGAAGAAAAATAATTTTCAAG 360
Qy 361 TCTTCTCTTTTCAGATGCTATTTGCTGCTCTGAGAAATTAAGAAAGCATGGC 420
Db 361 TCTTCTCTTTTCAGATGCTATTTGCTGCTCTGAGAAATTAAGAAAGCATGGC 420
Qy 421 AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAAATGGAAGAGCGCCCTAAAGAAACA 480
Db 421 AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAAATGGAAGAGCGCCCTAAAGAAACA 480
Qy 481 CCGATTCTGTTTCTATACAGCTGAAAAATTTTATAGTGGTGTCTTTTTTCCAGAAAGAG 540
Db 481 CCGATTCTGTTTCTATACAGCTGAAAAATTTTATAGTGGTGTCTTTTTTCCAGAAAGAG 540
Qy 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTTAAACACTATAGTGTGCGGAA 600
Db 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTTAAACACTATAGTGTGCGGAA 600
Qy 601 GAAACAGCGAAGCGCTTAAATACATTTTATGATCAAAAACCTTCAATCCTATGAAAT 660
Db 601 GAAACAGCGAAGCGCTTAAATACATTTTATGATCAAAAACCTTCAATCCTATGAAAT 660
Qy 661 AAGCGTGATTTTCTTATACAGATCAAAACGAGTCACTGTCTACTTTTTTAAAGAACGGGA 720
Db 661 AAGCGTGATTTTCTTATACAGATCAAAACGAGTCACTGTCTACTTTTTTAAAGAACGGGA 720
Qy 721 GAACTTTCGATTCGCACCAATTTGCGAAGAGCTTGCACTGTGCTCTAGCTTAAGTAAA 780
Db 721 GAACTTTCGATTCGCACCAATTTGCGAAGAGCTTGCACTGTGCTCTAGCTTAAGTAAA 780
Qy 781 GAAACCTTCAAAAAGAAATAGCTTGGCGACATTTTACAAATATGATCTATAGTGCCTT 840
Db 781 GAAACCTTCAAAAAGAAATAGCTTGGCGACATTTTACAAATATGATCTATAGTGCCTT 840
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Db 841 CCACAAACAAAAGAGGAGCTATTCAAGAAAAATTTTGGTTATATTTCAATGACACAAATGAC 900
Qy 901 CCAGAAATGTTTGTCAAGTGCAAAAGGGAGAGCGGGTACCCCTATTAATTTGATGCCGA 960
Db 901 CCAGAAATGTTTGTCAAGTGCAAAAGGGAGAGCGGGTACCCCTATTAATTTGATGCCGA 960
Qy 961 ATGCGACAACTGAATCAAACTGGTGGATGCACAAATCGCTTAAAGAAATGATTACTGCTCT 1020
Db 961 ATGCGACAACTGAATCAAACTGGTGGATGCACAAATCGCTTAAAGAAATGATTACTGCTCT 1020
Qy 1021 TTTTATAGTAAAAATTTACACATCGATTGGCGTTGGGGTGAAAAATACTTTTCAAAAAATG 1080
Db 1021 TTTTATAGTAAAAATTTACACATCGATTGGCGTTGGGGTGAAAAATACTTTTCAAAAAATG 1080
Qy 1081 TTGATTGACTATGATGCTGCCAATAATATCGTGGCTGGCAATGCGGCTGCTTCAACAGGA 1140
Db 1081 TTGATTGACTATGATGCTGCCAATAATATCGTGGCTGGCAATGCGGCTGCTTCAACAGGA 1140
Qy 1141 ACGGACGCTGTCCTTATTTTCGGATTTTAAATCCCAATTTTCCAGTCAAAAAATTTTAT 1200
Db 1141 ACGGACGCTGTCCTTATTTTCGGATTTTAAATCCCAATTTTCCAGTCAAAAAATTTTAT 1200
Qy 1201 AATGACGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCCACAAAAAGTAT 1260
Db 1201 AATGACGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCCACAAAAAGTAT 1260
Qy 1261 ATTCAATCAACAAATCTAATGAACGAAGCCCTTACAAACGCAATATCATGTACATTTAGGA 1320
Db 1261 ATTCAATCAACAAATCTAATGAACGAAGCCCTTACAAACGCAATATCATGTACATTTAGGA 1320
Qy 1321 GAAATTTATCAAAAACCAATTTGCTGATTTATGATCAAGTAAAAAACAACATTTGTTCTA 1380
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Db 1321 GAAATTTATCAAAAACCAATTTGCTGATTTATGATCAAGTAAAAAACAACATTTGTTCTA 1380
Qy 1381 TATGAAGCGAGCAAGAAATTCATCAAGAAATGAACAATCAAGGTTTCAATAA 1434
Db 1381 TATGAAGCGAGCAAGAAATTCATCAAGAAATGAACAATCAAGGTTTCAATAA 1434

RESULT 2
US-10-758-979-1
; Sequence 1, Application US/10758979
; Publication No. US20040214208A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Fredrick M.
; APPLICANT: Garsin, Danielle
; APPLICANT: Mylonakis, Eletherios
; APPLICANT: Calderwood, Stephen B.
; APPLICANT: Sifri, Costi
; TITLE OF INVENTION: Enterococcal Virulence Factors
; FILE REFERENCE: 00786/408002
; CURRENT APPLICATION NUMBER: US/10/758,979
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/22979
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,212
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2267
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-758-979-1

Query Match 100.0%; Score 1434; DB 8; Length 2267;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAAGAGTAATATGGTTTAGCGTATTACAGGATTACAGGATAATAAGGATTAGCA 60
Db 568 ATGAAAAGAGTAATATGGTTTAGCGTATTACAGGATAATAAGGATTAGCA 627
Qy 61 CAGCGGTTACAAAATTTCTGCAGCTGATGAATTTGATTTTATTTCCAAATGAATCTCTCAA 120
Db 628 CAGCGGTTACAAAATTTCTGCAGCTGATGAATTTTATTTCCAAATGAATCTCTCAA 687
Qy 121 CAATTTATTTCAAGAAAGTGTCTAATAACGCTTTTTTTTGCAGCTTAGCTCGTTCAAA 180
Db 688 CAATTTATTTCAAGAAAGTGTCTAATAACGCTTTTTTTTGCAGCTTAGCTCGTTCAAA 747
Qy 181 GAACGAATCGATCAAGAGGCACATTTTACAAATCATGCTCGGCGAACATTAGATTTATTT 240
Db 748 GAACGAATCGATCAAGAGGCACATTTTACAAATCATGCTCGGCGAACATTAGATTTATTT 807
Qy 241 TCAGGTTTCAAAACGCAAAATTTACCCGATTGCGAGCCATTTATTTTAAATGAAGACTTGT 300
Db 808 TCAGGTTTGAACGCAAAATTTACCCGATTGCGAGCCATTTATTTTAAATGAAGACTTGT 867
Qy 301 GGCCTTTGGGCAAGCGGACAGCAAGCTATGCGCTTTTTTGAAGAAAAATAATTTTCAAG 360
Db 868 GGCCTTTGGGCAAGCGGACAGCAAGCTATGCGCTTTTTTGAAGAAAAATAATTTTCAAG 927
Qy 361 TCTTCTCTTTTCAAGATGCTATTTTGCATGGCTCTGAAGAAATTAAGAAAGCATGGC 420
Db 928 TCTTCTCTTTTCAAGATGCTATTTTGCATGGCTCTGAAGAAATTAAGAAAGCATGGC 987
Qy 421 AGCAAGTACCAAGTGTTTTACGCCCTATTACAAATAAATGGAAGAGCGCCCTAAAGAAACA 480
Db 988 AGCAAGTACCAAGTGTTTTACGCCCTATTACAAATAAATGGAAGAGCGCCCTAAAGAAACA 1047
Qy 481 CCGATTCTGTTTCTTATACAGCTGAAAAATTTTATAGTGGTGTCTTTTTTCCAGAAAGAG 540
Db 1048 CCGATTCTGTTTCTTATACAGCTGAAAAATTTTATAGTGGTGTCTTTTTTCCAGAAAGAG 1107
```

ADDRESS: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 262:
SEQUENCE CHARACTERISTICS:
LENGTH: 5277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 262:
US-09-070-927A-262

Query Match 99.9%; Score 1432.8; DB 3; Length 5277;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1431; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAGAGTAATATGTTTAGCGTGTATACGATTACAGGATAATAAGCATTAGCA 60
DB 1046 ATGAAAAGAGTAATATGTTTAGCGTGTATACGATTACAGGATAATAAGCATTAGCA 1105
QY 61 CACCGTTACAAAATCTGCGAGCTGATGATTTTATTTTCCAAATGAATCCCTCAA 120
DB 1106 CACCGTTACAAAATCTGCGAGCTGATGATTTTATTTTCCAAATGAATCCCTCAA 1165
QY 121 CAATTTATTCAGAAAGTCTTAATCATACGCTTTTTCGAAGCTTAGCCTCGTTCAA 180
DB 1166 CAATTTATTCAGAAAGTCTTAATCATACGCTTTTTCGAAGCTTAGCCTCGTTCAA 1225
QY 181 GAACGAATCGATCAAGAGGCACTTTACAAATCATGTTCGGCGAACCAATAGATTTATTT 240
DB 1226 GAACGAATCGATCAAGAGGCACTTTACAAATCATGTTCGGCGAACCAATAGATTTATTT 1285
QY 241 TCAGCTTTGAAAACGCAAAATTACCCGATTTGGCAGGCAATTTATTTTGAAGATACCTTGT 300
DB 1286 TCAGCTTTGAAAACGCAAAATTACCCGATTTGGCAGGCAATTTATTTTGAAGATACCTTGT 1345
QY 301 GGCTTTGGGCAAGCGGACGACGACGCTATCGCTTTTTCGAAGAAATAATATTCAG 360
DB 1346 GGCTTTGGGCAAGCGGACGACGACGCTATCGCTTTTTCGAAGAAATAATATTCAG 1405
QY 361 TCTTTCTCTTTTCAAGATGCGCTATTTGATGGCTCTGGAAGAAATTAAGAGAACGATGGC 420
DB 1406 TCTTTCTCTTTTCAAGATGCGCTATTTGATGGCTCTGGAAGAAATTAAGAGAACGATGGC 1465
QY 421 AGCAAGTACCAAGTGTTTTACGCCCTTATTAATAATGGAAGAGGCCCTTAAAGAAACA 480
DB 1466 AGCAAGTACCAAGTGTTTTACGCCCTTATTAATAATGGAAGAGGCCCTTAAAGAAACA 1525

541 GAAGCAGCTTATCGTGACAGATTGCGAGGATTCCTTTAAACACACTATAGTGTGGCGAA 600
DB 1108 GAAGCAGCTTATCGTGAAACAGATTGCGAGGATTCCTTTAAACACACTATAGTGTGGCGAA 1167
QY 601 GAAACAGCCAGAGCGCGCTTAAATACTTTTATGATCAAAAACCTTCAATCTATGAAAT 660
DB 1168 GAAACAGCCAGAGCGCGCTTAAATACTTTTATGATCAAAAACCTTCAATCTATGAAAT 1227
QY 661 AAGCGTGATTTTCTTATCAGATCAAAACGAGTCACTGTCTACTTTTAAAGAACGGGA 720
DB 1228 AAGCGTGATTTTCTTATCAGATCAAAACGAGTCACTGTCTACTTTTAAAGAACGGGA 1287
QY 721 GAACTTTCGATTCGACCACTTTGGCAAGCTTGCATCTGTGCTTCTAGCTTAAGTAA 780
DB 1288 GAACTTTCGATTCGACCACTTTGGCAAGCTTGCATCTGTGCTTCTAGCTTAAGTAA 1347
QY 781 GAAACCTTTCAAAAAGAAATTAGCTTTGGCGCGACTTTTACAAATATGATCTATAGTGCCTTT 840
DB 1348 GAAACCTTTCAAAAAGAAATTAGCTTTGGCGCGACTTTTACAAATATGATCTATAGTGCCTTT 1407
QY 841 CCACAAACAAAAGAGGAAGCTATTCAAGAAAATTTCTGTATTTCAATGACAAAATGAC 900
DB 1408 CCACAAACAAAAGAGGAAGCTATTCAAGAAAATTTCTGTATTTCAATGACAAAATGAC 1467
QY 901 CCAGAAATGTTTGTCAAGTGGCAAAAAGGGGAGACGGGTACCTTAAATTTGATGCCGCA 960
DB 1468 CCAGAAATGTTTGTCAAGTGGCAAAAAGGGGAGACGGGTACCTTAAATTTGATGCCGCA 1527
QY 961 ATGCGACAACTGAATCAAACTGGTGGATGCACAAATCGCTTAAAGAAATGATTTACTGCTCT 1020
DB 1528 ATGCGACAACTGAATCAAACTGGTGGATGCACAAATCGCTTAAAGAAATGATTTACTGCTCT 1587
QY 1021 TTTTGTAGTTAAAAATTTACACATCGATTGGCGTGGGGTGAAAAATACTTTCAAAAATG 1080
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QY 1081 TTGATTGACTATGATCTGCCAATAATATATCGGTGGTGGCAATGGCTGCTTCAACAGGA 1140
DB 1648 TTGATTGACTATGATCTGCCAATAATATATCGGTGGTGGCAATGGCTGCTTCAACAGGA 1707
QY 1141 ACGGAGCTGCTCCCTTATTTTCGGATTTTTCGATTTTATCCAAATTTATCCAGTCAAAAAATTTGAT 1200
DB 1708 ACGGAGCTGCTCCCTTATTTTCGGATTTTTCGATTTTATCCAAATTTATCCAGTCAAAAAATTTGAT 1767
QY 1201 AATGACGGCCAGTTCAATCAAAAATATGTTCCAGAACTTTAAGCAAGTGCACAAAAGTAT 1260
DB 1768 AATGACGGCCAGTTCAATCAAAAATATGTTCCAGAACTTTAAGCAAGTGCACAAAAGTAT 1827
QY 1261 ATTCAATCAACCAATCTAATGAACGAGCTTTACAAACGCAATATCATGTATAGGA 1320
DB 1828 ATTCAATCAACCAATCTAATGAACGAGCTTTACAAACGCAATATCATGTATAGGA 1887
QY 1321 GAAATTTCCAAACCCATTTGCGATTATGATCAAGTAAAGAAACAAACATTTGTTCTA 1380
DB 1888 GAAATTTCCAAACCCATTTGCGATTATGATCAAGTAAAGAAACAAACATTTGTTCTA 1947
QY 1381 TATGAAGCGAGCAAGAAATTCATCAAGAAATGAACAATCCAAAGGTTTCAATAA 1434
DB 1948 TATGAAGCGAGCAAGAAATTCATCAAGAAATGAACAATCCAAAGGTTTCAATAA 2001

RESULT 3
US-09-070-927A-262
Sequence 262, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:

```

Qy 481 CCGATTCCTGTTTCTATACAGCTGAAGAAATTTTATAGTGGTGTCTTTTCCAGAGAG 540
Db 1526 CCGATTCCTGTTTCTATACAGCTGAAGAAATTTTATAGTGGTGTCTTTTCCAGAGAG 1585
Qy 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAAACACACTATAGTGTGCGGAA 600
Db 1586 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAAACACACTATAGTGTGCGGAA 1645
Qy 601 GAAACAGCAGAGCGCTTAAATCTTTTATGATCAAAACCTTCAATCTATGAAAT 660
Db 1646 GAAACAGCAGAGCGCTTAAATCTTTTATGATCAAAACCTTCAATCTATGAAAT 1705
Qy 661 AAGCGTGATTTTCTTATCAGATCAACAGAGTCTGTCTATCTTTTAAAGAACGGA 720
Db 1706 AAGCGTGATTTTCTTATCAGATCAACAGAGTCTGTCTATCTTTTAAAGAACGGA 1765
Qy 721 GAACTTTTCCGATTCGACCATTTGGCAAGAGCTTGCATCTGTGCTCTCTAGCTTAAATAA 780
Db 1766 GAACTTTTCCGATTCGACCATTTGGCAAGAGCTTGCATCTGTGCTCTCTAGCTTAAATAA 1825
Qy 781 GAAACCTTTCAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCTATAGTGGCTT 840
Db 1826 GAAACCTTTCAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCTATAGTGGCTT 1885
Qy 841 CCACACAAAGAGGAGCTATTCAAGAAATTTTCTTATATCAATGACACAAATGAC 900
Db 1886 CCACACAAAGAGGAGCTATTCAAGAAATTTTCTTATATCAATGACACAAATGAC 1945
Qy 901 CCAGAAATGTTTGTCAAGTGGCAAAAGGGGAGACGGGTACCCCTATAATTTGATGCGCA 960
Db 1946 CCAGAAATGTTTGTCAAGTGGCAAAAGGGGAGACGGGTACCCCTATAATTTGATGCGCA 2005
Qy 961 ATGGACAACTGAATCAAACTGGTTGGATGACAAATCGCTTAAAGATGATCTGCTCT 1020
Db 2006 ATGGACAACTGAATCAAACTGGTTGGATGACAAATCGCTTAAAGATGATCTGCTCT 2065
Qy 1021 TTTTGTAGTAAATTTTACATCGATTTGGGTTGGGTTGAAATATCTTCAAAATG 1080
Db 2066 TTTTGTAGTAAATTTTACATCGATTTGGGTTGGGTTGAAATATCTTCAAAATG 2125
Qy 1081 TTGATTGACTATGATGCTGCCAATAATATCGTGGCTGGCAATGGGCTGCTTCAACAGGA 1140
Db 2126 TTGATTGACTATGATGCTGCCAATAATATCGTGGCTGGCAATGGGCTGCTTCAACAGGA 2185
Qy 1141 ACGGACGCTGCTCTTATTTTCGGATTTTAAATCCAATATCCAGTCAAAATTTTGTAT 1200
Db 2186 ACGGACGCTGCTCTTATTTTCGGATTTTAAATCCAATATCCAGTCAAAATTTTGTAT 2245
Qy 1201 AATGACGCGCTTATCAAAATATGTTCCAGAACTTAAAGCAAGTGGCCACAAAGTAT 1260
Db 2246 AATGACGCGCTTATCAAAATATGTTCCAGAACTTAAAGCAAGTGGCCACAAAGTAT 2305
Qy 1261 ATTCAATCAACAAATCTAAATGAACGAGCTTACAAACGCAATATCATGTACATTTAGGA 1320
Db 2306 ATTCAATCAACAAATCTAAATGAACGAGCTTACAAACGCAATATCATGTACATTTAGGA 2365
Qy 1321 GAAATATCAAAACCCATTTGATGATGATGATCAAGTCAAGTCAAAACCAATGTTTCTA 1380
Db 2366 GAAATATCAAAACCCATTTGATGATGATGATCAAGTCAAGTCAAAACCAATGTTTCTA 2425
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Db 2426 TAKSAGCGAGCAAGAAATTCATCAAGAAATGAACAAATCCAGGTTTCAATA 2479

```

RESULT 4
 US-10-398-221-3604
 ; Sequence 3604, Application US/10398221
 ; Publication No. US200400185141
 ; GENERAL INFORMATION:
 ; APPLICANT: KUNST, Frederik
 ; APPLICANT: GLASER, Philippe

; TITLE OF INVENTION: Listeria innocua, genome and applications
 ; FILE REFERENCE: 344 702 - US
 ; CURRENT APPLICATION NUMBER: US/10/398,221
 ; CURRENT FILING DATE: 2003-03-27
 ; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 ; PRIOR FILING DATE: 2001-10-04
 ; PRIOR APPLICATION NUMBER: FR 00/12 697
 ; PRIOR FILING DATE: 2000-10-04
 ; NUMBER OF SEQ ID NOS: 4025
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3604
 ; LENGTH: 2460
 ; TYPE: DNA
 ; ORGANISM: Listeria monocytogenes 4b
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(end)
 ; OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
 US-10-398-221-3604

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Query Match      36.7%  Score 526.4;  DB 7;  Length 2460;
Best Local Similarity 61.6%  Pred. No. 4.9e-117;
Matches 883;  Conservative 0;  Mismatches 536;  Indels 15;  Gaps 2;

Qy 1 ATGAAAAGAGCTAATATATGTTTACAGCTGATTTACGATTACAGGATATAAAGCATTAGCA 60
Db 241 ATGACTTCGTAATATGTTTTCGAGAGATCTTCGAGTAAACGATATAAAGCTCTCTAT 300
Qy 61 CACGCGTTACAAAATTTCTGAGCTGATGAATGATTTATTTATTTCCAAATGAATCTCTCAA 120
Db 301 CATGC-----TTGTAAGAGGACGATTTGCTTTTGTATTTTCAAGTAATCCAGCA 351
Qy 121 CAATTTATTCAGAAAGTGTCTAATCATACAGCTTTTTTTTGCAGCTTAGCTCGTCTCAA 180
Db 352 CAGTTTCATCACAGAAAGTCTTAGCCACCAAGCTTTTTTTTGCAGAGTGGCTCATTTTAA 411
Qy 181 GAACGATTCGATCAAGAGGACATTTTACAAATCATGTGCGGCAACCATTAGATTTATTT 240
Db 412 CAAGAAATCGATAAAACTGCGCATTTTACAAATCATGTTGGTGAACCGATAGATGCTTC 471
Qy 241 TCACGTTTGAACCGCAAAATTACCCGATTGSCAGGCCATTTATTTTAAATGAAGATCTTGT 300
Db 472 CAACAACCTTAAAGATTCGCTACCAAGCTGGGATAAAGTTTATTTCAACCGTGAAGAA 531
Qy 301 GGCCTTTGGGCAAGCGGACAGCAAGCTATCGCTTTTTTTTGAAGAAATATATTCAG 360
Db 532 GSATACCGAGCAAGCGGATGAGCGGCGCAAGCGTTCTTTTGCAGCAACAAAATTCGAG 591
Qy 361 TCTTTCTCTTTTCAAGATGCTATTTTGCATGGCTCTGAAGAAATTAAGAAAGACGATGGC 420
Db 592 GTTCAAGCCTTCCAGATAGCTATCTTCAATGCGGAGAGAGTAAGAAATCTCCNACA 651
Qy 421 AGCAAGTCAACAAGTGTTTACGCCCTTATTAATAAATGGAAGAGGCGCTTAAAGAAACA 480
Db 652 GAATACTATAAAATTTTACCCCTTATATAAAATATGGCGGAAGAAATAAAGAAACG 711
Qy 481 CCGATTCCTGTTTCTTATACAGCTGAAATAATTTTATAGTGGCTGTCTTTTCCAGAGAG 540
Db 712 CCGTTCAAAAGTGAATTTTAAAGCATGAGAAATATCCGGAAGAAAGCTTTGTTTCTGA 771
Qy 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTTAAACACATATATAGTGTGCG 600
Db 772 GAAGAAATTTTCCGGAATGACT-----AGCGATTTACCGATNTAGATATTTGGTGA 825
Qy 601 GAAACAGCCAGAGGCGCTTAAATACTTTTATTTGATCAAAACCTTCAATCTATGAAAT 660
Db 826 CGAGCAGCGAAACACGAGACTTGGGAATTTTATTAACACGATGTTGCTGACTATGACAA 885
Qy 661 AAGCGTGATTTTCTTATCAGGATCAACAGGATCATCTGTCTACTTTTTTAAAGAACGGA 720
Db 886 GCGAGAGATTTTCCGGAACCTGGATAAAACAAGCATTATTCACGTTATTTACGACGGG 945
Qy 721 GAACTTTCGATTTCGCCACCATTTTGGCAAGAGCTTGCATCTGTGCTTCTTAGCTTTAA 780

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Db 946 GAAATCTCGATTGGACGATTTGGCGACATTTCAAGAAACAGAGCAACAGAGGACGA 1005
Qy 781 GAAACCTTTCAAAAAGAAATTAGCTTGGCGGCACTTTTACAATATATGATCTATAGTGGCTTT 840
Db 1006 GCTACATTTGAAAGAAAGCTGTGTAGGCGGCACTTTTATAATATGATTTACGCTTTCTTT 1065
Qy 841 CCACAAACAAAGAGAGAGCTATTCAAGAAATTTTCGTTATATTTCAATGACACAAATGAC 900
Db 1066 CCTAACCAAAACAGCGCGATCCAGAAATTTATCGTTTATTTGAATGGAAATTAAC 1125
Qy 901 CCAGAAATGTTGTCAAGTGGCAAAAGGGAGACGGGTACCCCTATATTAATTTGATGCCGA 960
Db 1126 CGCGAATATTTCAAGCGTGGCAGAGGGAAGACTGGTTCCCGCTGTTGATGGCGG 1185
Qy 961 ATGCAGCAACTGAATCAAACTGGTTGGATGCACAATCGCTTAAAGATGATTTACTGCGCTCT 1020
Db 1186 ATGCCCGAGTTGAAAGAACTGGTTGGATGCAATATCGAATCAAGAAATGATTTACGCGCTCC 1245
Qy 1021 TTTTGTAGTTAAATTTACACATCGATTTGGCGTTGGGTGGAATATCTTTCAAAAATG 1080
Db 1246 TTTTAAACAAAGATTTGCTGATTTGATTTGGCGTTTGGCGAAAGATTTTCAACAAATG 1305
Qy 1081 TTGATTGACTATGATGCTGCCAATATATCGGTGGCTGGCAATGGCTGCTTCAACAGGA 1140
Db 1306 CTGATTGATTATGATCTCGAGTAAATTTGGTGGCTGGCAATGGCGCTTCCGACTGA 1365
Qy 1141 ACGGACGCTGCTCCCTTATTTTCGGATTTTAAATCCAAATATCCAGTCAAAAATTTGAT 1200
Db 1366 ACGGATCGGTGCCATCTTTAGGATTTTCAACCCAAACAGACAAATCAACAAAATTTGAT 1425
Qy 1201 AATGACGGCAGTTGATCAAAAATATGTTCCAGAACTTTAGCAAGTGGCCACAAAGTAT 1260
Db 1426 TCGACTGGGAAATTTATTCGAAATATGTAAGAGATTTAGCGAATCTACCTGATAAATAT 1485
Qy 1261 ATTCATCAACCAATCTAATGAACGAGCTTTACAAACCAATATCATGTATCAATTTAGGA 1320
Db 1486 ATTCATCAACCAAGAAATGTCAGAACTGAGCAGAAAGACATGGCTTGTGTTAGGA 1545
Qy 1321 GAAATTTATCCAAACCCATTTGCGATTTATGATCAAGTAAAGAAACAAACATTTGTTCTA 1380
Db 1546 AAGACTATCCATTTCCGATAGTTGACCATTAAGACGAGCAATTTAGCCATTTGCACGC 1605
Qy 1381 TATGAAGCAGCAAGAAATTCATCAAGAAATGAACATCCAGGTTTCAATAA 1434
Db 1606 TACGAGTTTAGCAAGAGCACTTAGGGGAATATATAGATAATAGATCAATCA 1659

RESULT 5

US-10-398-221-10
; Sequence 10, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1163020
; TYPE: DNA
; ORGANISM: Listeria innocua
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u

US-10-398-221-10

Query Match 36.2%; Score 518.4; DB 7; Length 1163020;
Best Local Similarity 61.2%; Pred. No. 8.5e-114;
Matches 878; Conservative 0; Mismatches 541; Indels 15; Gaps 2;
Qy 1 ATGAAAGAGTAATATGTTTACAGCTGATTTACGATTTACGATTAAGAGCAATTAAGCAATTTAGCA 60
Db 537815 ATGACTTCAGTAATGTTTTCGTAGAGATCTTCGAGTAATAATGATATAAAGCTCTTTAT 537874
Qy 61 CAGCGTTTACAAAATCTCGAGCTGATGAATGATTTTATTTCCAAATGAATCCCTCAA 120
Db 537875 CATGCCCTGTAAGA-----AGAAAGATTAATTTGTTTATTTCAAGTAAATCCAGAA 537925
Qy 121 CAATTTATTCAGAAAGTGTCTAATCATACCGCTTTTTTTGCAAGCTTTAGCCTCTGCTCAAA 180
Db 537926 CAATTTATCAAGGAAGCCCTAGTCACCAAGCAATTTTCGCGAGTGTAGCTCATTTTCAA 537985
Qy 181 GAACGAATCGATCAAGAGGACATTTTACAAATCATGTCGGCGAACCATTAGATTTATTT 240
Db 537986 CAAGAACTAAATAAAAACACCCATTTTGCAAATCATGTTTGGCGAGCCAAATCGAGCTCCTA 538045
Qy 241 TCAGTTTGAACCCAAATTTACCGGATTTGGCAGGCCATTTATTTTAAATGAAGATACTTGT 300
Db 538046 AAACAATTTAAAGAAATAAATAACCAACTTTGGGATTAAGTTTTCCTCAACCGCGATGAACA 538105
Qy 301 GGCTTTGGGCAAGCGGACCCAGCAAGCTATGCGCTTTTTTTGAAGAAATAATATTTCAG 360
Db 538106 GGCTACGAGCGAGTCCAGACGAGGCTGCCGAGCAATCTTTGCTGATAAGGAATACACA 538165
Qy 361 TCTTTCTCTTTTCAAGATGCTTATTTGCATGGCTCTGAAAGAAATTTAGAAAGACGATGGC 420
Db 538166 GTTCACAGCTATCAGATAGTTTACCTTCATTCAGCTGAAGAGTGAATAATCCGCCACA 538225
Qy 421 AGCAAGTACCAAGTGTTTACGCCCTATATCAATTAATGGAAGAGCGCCCTAAAGAAACA 480
Db 538226 GAATACTACAAATCTTCACTCTCTTACTACAAAATAATGGCCGAGAAATAAAGAAATG 538285
Qy 481 CCGATTCCTGTTTCTTATACAGCTGAAATAATTTTATAGTGGCTGTCTTTTTCCAGAAAGAG 540
Db 538286 CCTTTAAAGTCACTTTTAAACAGAAATAATTAGGAAGAAAGCTTATTTCCAAATTTAT 538345
Qy 541 GAACGAGCTTATCGTGAACAGATTCGAGGATTCCTTTTAAACACATATAGTGTGGCGGAA 600
Db 538346 GAGGAACAGTTTACAGAACTGATTT-----CAAGATTTTACCAGCCTTTGATTTCCGGTGAA 538399
Qy 601 GAAACAGCAGAGCGCTTAAATCTTTTATTTGATCAAAACTTCAATCTCTATGAAAT 660
Db 538400 AAAGCAGCGAATACGAGACTTTGCAAACTTTGTAAGAAAGAGATTTAGCAGACTATGCAAA 538459
Qy 661 AAGCGTGAATTTTCTTATCAGGATCAACAGAGTCACTGTCTACTTTTTTAAAGAACGGGA 720
Db 538460 GCAAGAGACGTCGCCAGCGCTTGATTAACAGGATCAATTTATCAGCTATTTAGGAACGGGA 538519
Qy 721 GAACTTTTCGATTCGCACCAATTTGGCAAGAGCTTGCAATCTGTGCCCTTTAGCTTTAGTAAA 780
Db 538520 GAGATTTTCGATTCGTACGCTTTGGCAGGCACTTCAAAAAGAAAGAGCTACAGAGGACGA 538579
Qy 781 GAACTTTCAAAAAGAAATTTAGCTTTGGCGGCACTTTTCAATATCATCTATAGTGGCTTT 840
Db 538580 GCACATTTCAAAAAGAACTGTGTTGGCGCGATTTTATTAATATGATTTATGTTCTTTT 538639
Qy 841 CCACAAACAAAGAGAGGAGCTATTCAAGAAATAATTTTCGTTATTTTCAATGGAACAAATGAC 900
Db 538640 CCAAGCAAAAATAATGAGCCCTATTCAAGAAATAATTCGTTTATTTGAATGGAAATAAT 538699
Qy 901 CCAGAAATGTTTGTCAAGTGGCAAAAAGGGGAGACGGGTACCTTATTAATTTGATCCCGCA 960
Db 538700 CGCGAATTTTCAAGAGTGGCAAGCGGCAAACTGGTTTTTCCGCTTGTGATGCTGCG 538759
Qy 961 ATGCAGCAACTGAATCAAACTGGTTGGATGCACAATCCGCTTAAGAAATGATTTACTGCTCT 1020
Db 538760 ATGCGCCAAATTAAGAGACGGGCTGGATGCAATATCGGCTTAAGAAATGATTCACGGCTTCC 538819

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QY 1021 TTTTGTAGTTAAAAATTTACACATCGATTGGCGTTGGGGTGAATAATCTTTTCAAAAATG 1080
Db 538820 TTTTAAAGGAAGGATTTTACTAATTAATGATTGGCGTTTGGCGAAAAATATTTTCAACAAATG 538879
QY 1081 TTGATTGACTATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGA 1140
Db 538880 CTAATTGATTACGACCCAGCGANGTAATATTGGCGTTGGCAGTGGCGGCTTCGACTTGA 538939
QY 1141 ACGGACGCTGCCCTTATTTTCGGATTTTAAATCCAATTTATCCAGTCAAAAAATTTGAT 1200
Db 538940 ACAGATGCAGTACCGTATTTTAGAATTTTAAATCCAACCAACCAATCGGAAAAATTTGAT 538999
QY 1201 AATGACGCCAGTTTCATCAAAAATATGTTCCAGACTTAAGCACTTAAGCAAGTCCCAAAAGTAT 1260
Db 539000 CCAGATGGTACATTTATTTCGGAATATATGTAAGGAATTTACGGGACTTGC CGGATAAATTC 539059
QY 1261 ATTCAATCAACAAATCTAATGAACGAAGCCTTACAAACGCAATATCATGTACATTTTAGGA 1320
Db 539060 ATTCAATCAACGAAGAAATGCTGAAACAGACAGACAAAAGAGCATGGTTGATTTTAGGA 539119
QY 1321 GAAATATATCCAAACCCATTTGTCGATTTATGATCATCAAGTAAAGTAAACAAATGTTTCTA 1380
Db 539120 AAAGATTATCGCTTCCGATAATCGACCATAAAGAGCGACGAAAAATTAGCGATTGCGCGA 539179
QY 1381 TATGACGCGCAAGAATAATTCATCAAGAAATGAACATCCAGGTTTCAATA 1434
Db 539180 TATGAGTTTACGAAGGAGCATTTAGGGGAAATATATAGATAATGAATCAATCA 539233

RESULT 6
US-10-398-221-2058
; Sequence 2058, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398, 221
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2058
; LENGTH: 3011208
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-2058

Query Match 36.2%; Score 518.4; DB 7; Length 3011208;
Best Local Similarity 61.2%; Pred. No. 1.4e-113;
Matches 878; Conservative 0; Mismatches 541; Indels 15; Gaps 2;

QY 1 ATGAAAAGAGTAATATGGTTTATAGAGTATGATTTACGATTACAGGATAATAAGCAATTAGCA 60
Db 628080 ATGACTTCAGTAATATGGTTTTCGTAGAGATCTTCGAGTAATATGATAATAAGCTCTTTAT 628139
QY 61 CACGGTTACAAAATCTGCGAGCTGATGATTTGATTTTATTTATTCGAATGATCTCTCAA 120
Db 628140 CATGCCGTGTAAGA-----AGAAATTTAAATTTTGTATTTCGAAGTAAATCCAGAA 628190
QY 121 CAATTTATTCAGAAAGTGCTAAATCAAAACCTTTTTTTTGGCAAGCTTAGCGCTCGTTCAAA 180
Db 628191 CAATTTATCAAGGAAGCCCTAGTCACCAAGCATTTTTCGCGAGTGTAGCTCATTTTCAA 628250
QY 181 GAACGAATCGATCAAGAGGCACTTTTACAAATCATGTGCGCGAAACCATTTAGATTTATTT 240
Db 628251 CAAGAACTAAATAAAAAACCCCAATTTGCAATCATGTTTGGCGAGCCAAATCGAGCTCTTA 628310
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QY 241 TCACGTTTGAACGCAAAATTCACCGATTGGCAGGCCAATTTATTTTATGAAGATACATTGT 300
Db 628311 AAACAATTAAGAAAAAATACCAACTTGGGATAAAGTTTTTCTTCAACCGGATGAACA 628370
QY 301 GGCTTTGGGCAAGCGGACCAAGCTATGCGCTTTTGAAGAAAAATTAATATTTCAG 360
Db 628371 GGCTACGAGCGAGTCGAGACGAGGCTGCCGAGCATCTCTTCTGATAAGGAAATCAC 628430
QY 361 TCTTCTCTTTTCAAGATGCCATTTTGCATGGCTCTGAAGAAATTAAGAAAGACGATGGC 420
Db 628431 GTTTCAGAGCTATCACGATAGTTTACCTTCAATTCAGCTGAAGAGTGAATAATCCGCCA 628490
QY 421 AGCAAGTACCAAGTGTTTACGCCCTTATTAACAATAATGGAAGAGCGCCATAAGAAACA 480
Db 628491 GAATATCAAAAATCTTCACTCTCTTACAAAATTTGGCGCGAAGAAATTAAGAAATG 628550
QY 481 CCGATTCTCTGTTTCTATACAGCTGAAAAAATTTTATGTCGTGTCTTTTTCCAGAAAG 540
Db 628551 CCTTTAAAGTCACTTTAAAAACCGAAAAAATTTAGGAAGAAAGCTTATTTCCAAATTA 628610
QY 541 GAAGCAGCTTATCGTGAACAGATTGGAGGATTCCTTTTAAACACATATAGTGTGCGGAA 600
Db 628611 GAGGAACAGTTTATAGAACTGATT-----CAAGATTTTACAGCCTTTGATTCCGCTGAA 628664
QY 601 GAAACAGCCAGAGGCGCTTTAAATACTTTTATTGATCAAAAACTTCAATCTTATGAAAT 660
Db 628665 AAAGCAGCGAATACGAGACTTGCAAACTTTTGAAGAAAGATTTAGCAGACTATGACAAA 628724
QY 661 AAGCGTGATTTCTCTTATCAGGATCAACGAGTCATCTGTCTACTTTTTTAAAGACGGGA 720
Db 628725 GCAAGAGAGCTCCAGCGCTTGATAAAACGAGTCACTTATCACGCTATTTACGAACGGGA 628784
QY 721 GAATTTTCGATTCGCAACCATTTGGCAAGAGCTTGCATCTGTGCTTCTAGCTTAAAGTAA 780
Db 628785 GAGATTTTCGATTCGCTGCTTGGCAGGCACTTTCAAAAAAGAAAGCTACAGAAAGGACGA 628844
QY 781 GAAACCTTCAAAAAAGAAATTTAGCTTCGCGGACCTTTTACAAATATGATCTATAGTGCCTT 840
Db 628845 GCAACATTCGAAAAGAACTGTGTTGCGCGGATTTTATATATGATTTATGTTCTTTT 628904
QY 841 CCACAAACAAAAGAGGAAGCTATTTCAAGAAAAATTTTCGTTATATTCAATGACACAAATGAC 900
Db 628905 CCAAGCAAAAAAATGAGCCTATTTCAAGAAAAATTCGTTTATTTGAATCGGAAAAAT 628964
QY 901 CCAGAAATGTTTGTCAAGTGGCAAAAGGGGACCGGGTACCTATATTTGATGCGGCA 960
Db 628965 CGCGAATTTTTCAGGAAGTGGCAAGCGGGCAAACTGGTTTTCCGCTTGTGATGCTGCG 629024
QY 961 ATGCGCAACTGAATCAAACTGGTGGATGCAAAATCGCTTAAAGAAATGATTACTGCTCT 1020
Db 629025 ATGCGCAATTAAGAGAGCGGCTGGATGCAATTCGGCTAAGAAATGATCACGGCTTCC 629084
QY 1021 TTTTATAGTTAAAAATTTTACACATCGATTGGCGTTGGGGTGAATAATCTTTTCAAAAAATG 1080
Db 629085 TTTTAAACGAAGGATTTTACTAATTTGATTTGGCGTTTTTGGGAAAAATATTTTCAACAAATG 629144
QY 1081 TTGATTGACTATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGA 1140
Db 629145 CTAATTTGATTTACGACCCAGCGAGTAATATTGGCGGTTGGCAGTGGGCGGCTTCGACTGGA 629204
QY 1141 ACGGACGCTGCTCTTATTTTCGATTTTAAATCTCAATTTATCCAGTCAAAAAATTTGAT 1200
Db 629205 ACAGATGCAGTACCGTATTTTAGAATTTTAAATTCACCAACCAATTCGGAAAAATTTGAT 629264
QY 1201 AATGACGCCAGTTCATCAAAAAATATGTTTCCAGAACTTAAGCAAGTCCCAAAAAAGTAT 1260
Db 629265 CCAGATGGTACATTTATTCGGAATAATGTAAGAAATTTACGGGACTTCCGGGATAAATTC 629324
QY 1261 ATTCAATCAACAAATCTAATGAACGAGCCTTCAACACGCAATATCATGTACATTTAGGA 1320
Db 629325 ATTCAATCAACCAAAAAAATGCTGAAACAGAGCAAAAAAGAGCATGGTTGATTTTAGGA 629384
QY 1321 GAAATTTATCCAAAAACCCATTTGTCGATTTATGCAATCAAGTAAAAAACAACATTTGTTCTA 1380
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Db 629385 AAAGATTATCGCTTCGATTAATCGACCAATAAGAGCGGACGAAATTAGCGATTGCGGA 629444
 Qy 1381 TATGAAGCGAGCAAGAAATTCATCAAGAAATGAACAAATCCAGGTTTCAATAA 1434
 Db 629445 TATGAGTTTAGCAAGGAGCAATTCCTAGGGGAAATATATAGATAATGAATCAATCA 629498

RESULT 7

US-10-398-221-1690
 ; Sequence 1690, Application US/10398221
 ; Publication No. US20040018514A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KUNST, Frederik
 ; TITLE OF INVENTION: Listeria innocua, genome and applications
 ; FILE REFERENCE: 344 702 - US
 ; CURRENT APPLICATION NUMBER: US/10/398,221
 ; CURRENT FILING DATE: 2003-03-27
 ; PRIOR FILING DATE: 2001-10-04
 ; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: FR 00/12 697
 ; NUMBER OF SEQ ID NOS: 4025
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1690
 ; LENGTH: 1451
 ; TYPE: DNA
 ; ORGANISM: Listeria monocytogenes-4B
 US-10-398-221-1690

Query Match 29.1%; Score 416.8; DB 7; Length 1451;
 Best Local Similarity 59.0%; Pred. No. 1.6e-90;
 Matches 759; Conservative 0; Mismatches 512; Indels 15; Gaps 2;

Qy 1 ATGAAAGAGTAATATGGTTTATAGAGCTGATTTACGATTACAGGATAATAAGCAATTAGCA 60
 Db 39 ATGACTTCGGTANTGGTTTCGGAGAGATCTTCAGTAACGATAATAAGCTCTCTAT 98
 Qy 61 CACGGGTTACAAAATTCAGCTGATGAATGATTTATATATCCAAATGAATCCTCAA 120
 Db 99 CATGC-----TTGTAAGAGAGGAGCAGATTTGCTTTTGTATTTCAAGTAATCCAGCA 149
 Qy 121 CAATTTATTCAGAAAGTCTTAATCATACGCTTTTTTTTGGCAAGCTTAGCCTCGTTCAA 180
 Db 150 CAGTTTCATCAGGAAGTCTTAGCCACCAAGCTTTTTTTTGGCAAGTGTGGCTCATTTTAAG 209
 Qy 181 GAACGATCGATCAGAGGACATTTACAAATCATGTCGCGGCAACCATTTAGATTTATTT 240
 Db 210 CAAGAAATCGATAAAACTCGGCATTTTACAAATCATGTTTGGTGAACCGATAGATGCTTC 269
 Qy 241 TCACGTTTCAAAACGCAAAATTTACCGATTTGGCAGGCCATTTATTTAATGAAGATCTGT 300
 Db 270 CAACAACTTAAGATTCGCTACCAAGCTGGGATAAAGTTTATTTCAACCGTATGAACA 329
 Qy 301 GCGTTTGGGCAAGAGCGGACAGCAAGCTATGCGCTTTTTTGAAGAAATTAATTTCAAG 360
 Db 330 GGATACGAGCAAGAGCGGATGAGCGGCGCAAGCGTTCTTTGACGACAAAATAATCGAG 389
 Qy 361 TCTTTCTCTTTCAAGATCGCTATTTGTCATGCTCTGAAGAAATTAAGAAAGAACGATGCG 420
 Db 390 GTTCAAGCGCTTCACGATAGTATCTTCATTCAGCGAAGAGTAAGAAATCTCCACA 449
 Qy 421 AGCAAGTACCAAGTGTTTAGCCCTATTACAAATAATGGAAGAGCGCGCTAAAGAAACA 480
 Db 450 GAATCTATAAATTTTACCCCTTATTATAAAATATGGCGAAGAAATAAGAAAGCG 509
 Qy 481 CCGATTCCTGTTTCCATATACAGCTGAAAAATTTTATAGTCGCTGCTTTTCCAGAGAG 540
 Db 510 CCGTTCAAGTGTCTTAAAGCATGAGAAATATCCGGAAAGAAAGCTTGTCTTGAATAT 569
 Qy 541 GAAGCAGCTTATCGTGAACAGATTCGAGGATTCCTTTTAAACACACTATAGTGTGCGGAA 600

Db 570 GAAGAAACAATTCGCGAAATGACT-----AGCGATTTACCGATATATAGATATTGGTGAA 623
 Qy 601 GAAACAGCGAGAGGCGCTTAAATACTTTTATTTGATCAAAAACTTCAATCCTATGAAAAAT 660
 Db 624 CGAGCAGCGAACACAGAGACTTGGGAATTTTATTAACACAGATGTGCTGACTATGACAAA 683
 Qy 661 AAGCGTGAATTTCTTATCAGGATCAACAGAGTCATCTGCTACTTTTAAAGAACGGGA 720
 Db 684 CGAGAGATTTCCCGGAACCTGGATAAAACAAGCCATTTATCAGCTTATTTACGAACGGGG 743
 Qy 721 GAATCTTCGATTCGCACCACTTTTTCGCAAGAGCTTTCATCTGCTGCTTCTAGCTTTAAGTAAA 780
 Db 744 GAAATCTCGATTCGAGCGATTTTTCGAGACACTTCAAGAAACAGACGAAACAGAGAGGACA 803
 Qy 781 GAAACCTTTCAAAAAAGAAATTTAGCTTTCGCGGAGCTTTTACAAATATGATCTATAGTGCCTTT 840
 Db 804 GCTACATTTGAAAAAGAACTGTGTAGCGCGAGCTTTTATAATATGATTTACGTTCTCTTT 863
 Qy 841 CCACAAACAAAAAGAGGAGCTATTTCAAGAAAAATTTTCGTTTATTTCAATGACACAAATGAC 900
 Db 864 CTTAAACCAAAAAACGAGCGGATCCAGAAAAATTTATCGTTTATTTGAATGGGAAAAATAAC 923
 Qy 901 CCAGAAATGTTTGTCAAGTCGCAAAAGGAGGAGCGGTACCCCTATAATTTGATGCGCGCA 960
 Db 924 CGCGAATATTTCAAGAGCTGGCAAGATGGGAAGAGCTGTTTCCGCTCGTTGATGCGGTG 983
 Qy 961 ATGCGCAACTGAAATCAAACTGGTTGGATGCACAACTCGTTTAAAGAAATGATTTACTGCTCT 1020
 Db 984 ATGCGCCAGTTGCAAGAACTGGTGGTGCATCATGAGTACGACTAGAACTGTTTACGCTGACC 1043
 Qy 1021 TTTTAGTTAAAAATTTACATCATGATTCGCTTGGGTGGGTGAAATAATCTTTTCAAAAAATG 1080
 Db 1044 TTTTAAACAAAGGATTTAGTTAGTGGCGGATTTGTCGAGAAAGCTTTTTTCTTCAACTG 1103
 Qy 1081 TTGATTCAGTATGATGCTCCCAATAATATCGTGGCTGGCAATGGCTGCTTCAACAGGA 1140
 Db 1104 CTGATGATTTCTGATCTCTGCGAGTCATATCGGGGCTGGCAATGGCGGCTTCACTGGC 1163
 Qy 1141 ACAGACCTGTCCTCTATTTTCGGATTTTAAATCCAAATTTATCCAGTCAAAAAATTTGAT 1200
 Db 1164 ACAGTGGGGCCATCTATTTATGATCTTCAACGGAGCTGCTGCGCAATTCCT 1223
 Qy 1201 AATGACGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAAGCAAGTGCACAAAGTAT 1260
 Db 1224 TCCCTCGGAAATTCATTTACCAATACTGCGCATGATTTGGCGAATCTGCTGCTGCTTAT 1283
 Qy 1261 ATTCAATCAACCAATCTTAATGAACGA 1286
 Db 1284 CTCCATGCTCCATACACTGCCCCGA 1309

RESULT 8

US-08-781-986A-594
 ; Sequence 594, Application US/08781986A
 ; Publication No. US20030054436A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Kunsch
 ; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 ; NUMBER OF SEQUENCES: 5255
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 ; COMPUTER: Hp Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/781,986A


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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 594:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1393 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-594

Query Match      14.4%; Score 206.2; DB 2; Length 1393;
Best Local Similarity 56.2%; Pred. No. 2.3e-39;
Matches 432; Conservative 0; Mismatches 328; Indels 9; Gaps 2;

QY 627 TTTTATTGATCAAAACCTTCAATCCTATGAAATAAGCGTGATTTTCCTTATCAGGATCA 686
DB 617 TTTTATTGATCAAGATATACAGAATTACGAAGCGGAGAGACTATTTACCTGAAGTATT 676
QY 687 AACGAGTCATCTGCTACTTTTAAAGAACGGGAGAACTTTCGATTTCGCACCATTTTGGCA 746
DB 677 AACAGTCAGCTAAGTGTGCTTTAGCATATGGATTATTAGATATTATTGAAATTTTAA 736
QY 747 AGA-----GCTTGCATCTGCGCTTCTAGCTTAAGTAAAGAAACCTTCAAAAAGAAATT 800
DB 737 TGATTTATTGGCGGCTTATGATGAAGATGAGGCAAACTATCAAGCAITTTATACGTGAAT 796
QY 801 AGCTTGGCGGACCTTTTACAAATATGATCTATAGTGGCTTTCCACAAACAAAAGGGAAGC 860
DB 797 CATTTTATAGAGATTTTATTATGTGTTAATGACACAGATCTCTGAAACCTCATACCAAGC 856
QY 861 TATTCAAGAAAAATTTCTGTTATATTCATGACAAATGACCCAGAAATGTTTGCAAGTG 920
DB 857 TTTCAACCTTAATATCGACAGATAAATGTCGCAAAATGAAGCGGATTTAATGATG 916
QY 921 GCAAAAAGGGGAGACGGGGTACCCTATAATTAATGATGCCGCAATGCGAATCGAATCAAAC 980
DB 917 GTGCGAAGGGCAACACAGGATTTCCAATCATTTGATGTCAGCAATAATGGAATTCACACAAAC 976
QY 981 TGGTTGGATGCACATCGCTTAAGAATGATTACTGCGCTCTTTTATTAGTTAAATAATTACA 1040
DB 977 TGGTTTATGCAATAATCGAATGAGAATGGTTGTGTCGCAATTTTAAACCAAGATTTATT 1036
QY 1041 CATCGATTGGCGTTGGGGTGAAAAATACTTTCAAAAAATGTTGATTGACTATGATGCTG 1100
DB 1037 TATAGATTGGACATGGGGAGAAAAATTTCTTAGAAGACCTTATTGACTATGATGAGC 1096
QY 1101 CAATAATATCGTGGCTGGCAATGGCTGCTTCAACAGGAACGGACGCTGTCCTTATTT 1160
DB 1097 ATCAAAATATTATCGATGGCAATGGTCTGCTTCTACAGGTACGGATGCGATGCGCGTATTT 1156
QY 1161 TCGGATTTTAAATCCCAATTATCCAGTCAAAAAATTTGATAATGACGCGCAGTTTCATCA 1220
DB 1157 TAGAATGTTTAAATCCCAATAAGACAGAGTGAAACGCTTTGATGCTTAAAGCTTTGTATATCA 1216
QY 1221 AAAATATGTTCCGAACTTAAAGCAAGTGCCACAAAAGTATATTATCATCAACCAAAATCTAAT 1280
DB 1217 AACATATCTCCGATTTTAAATCAAAATGATGCAAAATATTGTCATGATACA---CAAGC 1273
QY 1281 GAACGAAGCCCTTACAAACGCAATATCATGTACATTTTAGGAGAAATTTATCCAAACCCAT 1340
DB 1274 CAATGAGTCCAAACCTTTTGAACAGGGGATTTGAATTAGGTAGTCAATTATCCAAAGACAAAT 1333
QY 1341 TGTGATTTATGCATCAAGTAAAAAACAACATTTGTTTCTATATGAAGCG 1389
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DB 1334 GGTAGATCATCAAGAAAAACGTACAAAGTTTTAGCTACATTTTAAAGCG 1382

RESULT 9
US-10-329-624-594
; Sequence 594, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248PID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 594:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1393 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 594:
US-10-329-624-594
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Query Match      14.4%; Score 206.2; DB 7; Length 1393;
Best Local Similarity 56.2%; Pred. No. 2.3e-39;
Matches 432; Conservative 0; Mismatches 328; Indels 9; Gaps 2;
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QY 627 TTTTATTGATCAAAAACTTCAATCCTTATGAAATAAGCGTGATTTTCCTTATCAGGATCA 686
DB 617 TTTTATTGATCAAGATATACAGAATTACGAAGCGGAGAGACTATTTACCTGAAGTATT 676
QY 687 AACGAGTCATCTGCTACTTTTAAAGAACGGGAGAACTTTTCGATTTCGCACCATTTTGGCA 746
DB 677 AACAGTCAGCTAAGTGTGCTTTAGCATATGGATTATTAGATATTATTGAAATTTTAA 736
QY 747 AGA-----GCTTGCATCTGTCCTTCTAGCTTAAGTAAAGAAACCTTCAAAAAGAAATT 800
DB 737 TGATTTATTGGCGGCTTATGATGAAGATGAGGCAAACTATGAAGCAITTTATACGTGAAT 796
QY 801 AGCTTGGCGGACCTTTTACAAATATGATCTATAGTGGCTTTCCACAAACAAAAGGGAAGC 860
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Db 797 CATTTTATAGAAATTTTATTATGTTTAAATGACACAGTATCCTGAAACCTCATACCAAGC 856
Qy 861 TATTCAAGAAAATTTGTTTATTTCAATGAGCAAAATGACCAGAAATGTTTTCAGTG 920
Db 857 TTTCAAACTAAATATCGACAGATAAAATGTCGCAAAATGAAGCGGATTTTAAATGCATG 916
Qy 921 GCAAAAGGGAGAGCGGTACCTTATATGATGCGCAATGCGACAATGGAATCAAAAC 980
Db 917 GTGCAAGGGGCAACAGGATTTCCATCATTTGATGCGACCAATATGGAATTTGACACAAC 976
Qy 981 TGGTTGGATGCACAATCGCTTAAAGAAATGATTAATGCTCTTTTTCAGTTAAATAATTTACA 1040
Db 977 TGGTTTATGCATATATCGAATGAGAATGTTGTCGCAATTTTAAACCAAGATTTATT 1036
Qy 1041 CATCGATTGGCGTTGGGTGAAAAATACCTTCAAAAAATGTTGATTTGACTATGATGCTGC 1100
Db 1037 TATGATTGGACATGGGAGAAAAATCTTTAGAAAAGCACCTTATTTGACTATGATGCGAGC 1096
Qy 1101 CAAATATATCGGTGCTGCAATGCTCTTCAACAGCAAGCGAGCTGCTCCCTTATTT 1160
Db 1097 ATCAAAATATTCATGATGGCAATGCTGCTTCTACAGTACGGATGCGATGCGGTATTT 1156
Qy 1161 TCGGATTTTATCCAAATATCCAGTCAAAAAATTTGATATGACGGCCAGTTTCATCAA 1220
Db 1157 TAGAATGTTTATCCAAATAGACAGATGAACGCTTTGATGCTAAGCTTTGTATATCAA 1216
Qy 1221 AAAATATGTTCCAGAACTTAAAGCAAGTGCACAAAGTATATTTCAACCAAAATCTTAAT 1280
Db 1217 ACATATATCTCCGATTTTAAATCAAAATGATGCAAAATATTTGCAATGATACA--CAAGC 1273
Qy 1281 GAACGAGCTTACAAACCAATATCATGATATTTAGGAGAAATTTTCAAAACCCAT 1340
Db 1274 CAATGAGTCCAACTTTTGAACAGGGGATGAAATAGGTATGCTCAATTTCCAAAGCAAT 1333
Qy 1341 TGTGATTATGATCAAGTAAAAAAACAAACATTTGTTTCTATATGAAGCG 1389
Db 1334 GGTAGATCATCAAGAAAACGTACACAGTTTATGCTACATTTTAAAGCG 1382

RESULT 10

US-10-724-972A-3359
; Sequence 3359, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PAT03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; PRIOR FILING DATE: 2003-12-01
; CURRENT FILING DATE: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 3359
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: S. epidermidis
US-10-724-972A-3359

Query Match 13.9%; Score 199; DB 7; Length 1380;
Best Local Similarity 58.9%; Pred. No. 1.3e-37;
Matches 362; Conservative 0; Mismatches 250; Indels 3; Gaps 1;
Qy 774 AAGTAAGAACCTTCAAAAAAGAAATAGCTTCGGCGAGCTTTTACAAATATGATCTATAG 833
Db 759 AAATACGAAACTTTTATACGTGAATTTTATAGAGATTTTATATGATTAATGAC 818

Qy 834 TGGTTTTCCACAAACAAAGAGGAAGCTATTTCAAGAAAAATTTCTGTTATATTTCAATGGAC 893
Db 819 CAATTATCCGNAACAGCTCATGTTGCTTTTAAAGAAAAATACCAAAATTTGAAATGGTC 878
Qy 894 AATGACCCAGAAATTTTGTCAAGTGGCAAAAAAGGGAGACGGGTACCTTAATTTGA 953
Db 879 TTATAATGAAGAGAAATTTTAAACTGTGGAAGATGGAATCTACTGTTTTCATATTTGA 938
Qy 954 TGGCGCAATCGCAACACTGAATCAAACTGGTTGATGCACAATCGCTTAAAGAAATGATTAC 1013
Db 939 TGCAGCAATGGAGAACTTAAACAACTGGAATTTATGCAATATCGCATGAGATGGTAGT 998
Qy 1014 TGCCTCTTTTATAGTTAAAAATTTTACATCGATGCGTTGGCGTTGGGGTGAATAACTTTTCA 1073
Db 999 TTCTCAATTTTAACTAAAGATTTGTTTATTGACTGGATTTGGGGTGAATCAATTTTCAA 1058
Qy 1074 AAAAATGTTGATGACTATGATGCTGCAATATATCGTGGCTGCGCAATGGCGTGTTC 1133
Db 1059 AAAAAATTAATAGATTTATGATGCGAGCTTCAATGTTTTCAGGATGGCAGTGGTCAGCTTC 1118
Qy 1134 AACAGGAACGAGCGCTGCTCTTATTTTCGGATTTTAAATCCAATTTTCAAGTCAAAAA 1193
Db 1119 TACTGGAACAGATGCTGTACCACTTTTAGAATGTTTAAATCTTATAGACAAGCGAGCG 1178
Qy 1194 ATTTGATAATGACGGCCAGCTTCATCAAAAAATATGTTTCCAGAACTTAAAGCAAGTGCACA 1253
Db 1179 TTTTGTATATAATGACGATATATAAAATTTACATTTCCAAAGATTTAAATCAGGTAGATGC 1238
Qy 1254 AAAGTATATTCATCAACCAAAATCTAATGAAGCAAGCCCTTACAAAGCNAATCATGTACA 1313
Db 1239 TAAGTATTTACAGCATACTCATAAATTCGAGCAACAAATAAAGGGGCAA---GGTGTGA 1295
Qy 1314 TTTAGGAGAAATTTATCCAAACCCATTTGCTGATTATGCTCAATGAAATTAAGCAAAACAT 1373
Db 1296 AATAGGTAAGACTATCTTAAACAAATGATTGATCAAAAGAAATGATGACAAACGTTAAT 1355
Qy 1374 GTTTCTATATGAAGC 1388
Db 1356 GTCAGATTCAAAGC 1370

RESULT 11

US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 12.9%; Score 184.8; DB 3; Length 640681;
Best Local Similarity 54.2%; Pred. No. 7.4e-33;
Matches 465; Conservative 0; Mismatches 357; Indels 36; Gaps 3;
Qy 572 TTCCTTTTAAACACACTATATAGTTCGCGGAAGAAACAGCCAGAGCGCTTAATACTTTTA 631
Db 331419 TTAATAAAAAATTTCTTCTCTGTTGGAGAAAAAGAGGCTATTAAATCGTTTAAAAAATTTT 331478

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QY 632 TTGATCAAAACCTCAATCTCTAGTAAATAAGCGTGATTTTCCCTTATCAGGATCAAAACGA 691
Db 331479 GTATATATAAATTAATGATTAATTTCTTAACAGAGATATCCCTTTTATAGATCTACTA 331538
QY 692 GTCATCTGTCTACTTTTAAAGAACGGGAGAACTTTTCGATTCGACCAATTTGGCAAGAGC 751
Db 331539 GTATGCTGTCTCCATATTTATCAGCAGGAATAATCATCTCGATATTTGTCTTAAAGTGC 331598
QY 752 TTG-----CATCTGTGCTCTAGCTTAAGTAAAGAAACCTTCAAAAAGAA 798
Db 331599 TTTTAAAAACAAAACAGCTCTCCATTAATGTCTTCTTACGTCTCTGTGTTTGATC 331658
QY 799 TTAGCTTGGCGAGCTTTTACAATATGATCTATAGTGTGTTTCCACAAACAAAAGAGAA 858
Db 331659 AGATATATGCGTGAAATTTTATACCATTTTAAATTTGATTTCCAAAATTTAGTAGAT 331718
QY 859 GCTATTCAAGAAAAATTTTCG-----TTATATTCAATGAGCAAAATGACCCGAAATGTTTG 913
Db 331719 CTGAATCATATTAGTAAATGCGGAAAAAGAAATTCATTTGATATAATAATAAAACATTTTA 331778
QY 914 TCAAGTGGCAAAAGGGAGAGCGGGGTACCTTAATATGATGCGCGAATGGGCAACTGA 973
Db 331779 ATGCTGCGAAAGAGAAATACAGGTTTTCCTATAATAGATGCAAGAAATGAGACAAATTA 331838
QY 974 ATCAAACTGGTTGGATGACAACTCGCTTAAGAATGATTACTGCTCTTTTCTAGTTAAAA 1033
Db 331839 ACGAATGAGATGATGATTAATTAAGATTAATTAAGATTAATTAAGATTTTCTAGTTAAAA 331898
QY 1034 ATTTACACATCGATTGGCGTTGGGGTGAATAATATCTTTCAAAAAATGTTGATGACTATG 1093
Db 331899 ATCTTTTGATTAATTGGCGAGAGGGGAGAACTTTTATATCTAATTAATGATGGAG 331958
QY 1094 ATGCTGCAATAATATCGTGGCTGGCAATGGGCTGTTCAACAGGACGACCTGTCC 1153
Db 331959 ACTTAGCGCTGAATAATGAGGATGGCAATGCTCAGCGTCAAGTGGGATGTTCTGTAC 332018
QY 1154 CTTATTTTCGATTTTAAATCCATTTATCCAGTCAAAAAATTTGATAATGAGCGGCAGT 1213
Db 332019 CTTATATAAGAAATTTTAAATCCATTTACATCAATCAAAAACTTTTGTAGTAATCGGGTAAT 332078
QY 1214 TCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCACAAAAGTATATATTCATCAACCAA 1273
Db 332079 TTATAAGAGAAGTTTATACCAAGAAATTAAGAAACGGTCTTAATCATCATCAACCAAC 332138
QY 1274 ATCTAATGAACGAAGCCTTACAAAGCAATATCATGATACATTTAGGAGAAATTTATCAA 1333
Db 332139 AT-----GAAATGGTCAAAACAAAAAAATTTTAAAAATAGATTTATCCTA 332180
QY 1334 AACCCATTGTCGATTATGTCATCAAGTAAACAAAACAAACATTTCTTATATGAACGAGCA 1393
Db 332181 ATCCTATTATTAATTTATAGTGAAGCAAGCAAAAAACATCTTTATCGCTATTCAACAGCTC 332240
QY 1394 AAGAAATTCATCAAGAA 1411
Db 332241 GATTAAACCTCATAAA 332258
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RESULT 12

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US-10-793-639-226
; Sequence 226, Application US/10793639
; Publication No. US20040199940A1
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 16516-075
; CURRENT APPLICATION NUMBER: US/10793,639
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US/09/614,221A
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/142,981
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; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 226
; LENGTH: 1698
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-793-639-226
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Query Match 9.6%; Score 137.2; DB 8; Length 1698;
Best Local Similarity 57.6%; Pred. No. 1.5e-22;
Matches 266; Conservative 0; Mismatches 193; Indels 3; Gaps 1;

QY 782 AAACCTTCAAAAAAGAAATAGCTTGGCGGACATTTTACACAA--ATATGATCATATAGTGCCT 838
Db 1136 AAATTTTCATCAAGAAGTTGCAATGAGAGATTTTACAGACATTTGATGCTGCACTGGC 1195
QY 839 TTCCACAAACAAAAGAGAAAGCTTATTCAAGAAAAAATTTTCGTTATATTTCAATGGACAAATG 898
Db 1196 CATATACCTCAATGGGAATGCCCTTATCGATTGGACACTTTTAGATATAAAAAATGGAGAATA 1255
QY 899 ACCAGAAATGTTTGTCAAGTGCACAAAAGGGAGAGCGGGTACCTATATATTTGATGCGCG 958
Db 1256 ACCCTGTAGCAATTTGAAAAAGTGTGTACTGTTAATACAGGCATTTCCCATAGTCGATGCCA 1315
QY 959 CAATGCGACAACTGAATCAAACTGGTTGGATGCACAAATCGCTTAAAGAAATGATTACTGCT 1018
Db 1316 TAAAGAAAAATTTACTGTACAGGCTATTTAATTAACAGATCTAGATGATCAGACTT 1375
QY 1019 CTTTTTTAGTTAAAAATTTTACACATCGATTTGGCGTTGGGTGAAAAAATACTTTCAAAAAA 1078
Db 1376 CTTTTCTTTCTAAAAAATTTAATTAATAGATTGGAGATGGGGGAAACGCTGTTTATGAAAC 1435
QY 1079 TGTGATTTGATGATGATGCTGCCAATAATATCGTGGCTGGCAATGGGCTGCTTCAACAG 1138
Db 1436 ACTTGTAGACGCTGATTCGTTCTTCAAAATGTTGGTGGCTGGGGTTTTGTCTTAGTACAG 1495
QY 1139 GAACGACGCTGTCCTTATTTTCGGATTTTTCGGATTTTAAATCCAAATATCCAGTCAAAAAATTTG 1198
Db 1496 GAATTGATGCCCAACCATATTTTAGAGTTTTTATGATATACAGCAAAAAAATATG 1555
QY 1199 ATAATGACGGCCAGTTTCATCAAAAAAATATGTTTCCAGAACTTA 1240
Db 1556 ACCCACAAATGATATTTCGTCAAAACAAATGGTTCCCGAATTGA 1597
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RESULT 13

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US-09-738-626-701
; Sequence 701, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 701
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642957	TGGCGTGCAGAAAAACAGGAATTC	CGCGTGCAGCGATCGGAGAA	TTATCGGCGC	642899
979	ACTGGTGGATGCACATCCGCTTA	AGAAATGATTACTGCCTCT	TTTTTTTAGTTAAAAATTTA	1038
642897	ACCGGGTCAATGCACAAATCGCGT	CAGAAATGGTAGTAGTCTAT	TTTTTTTAAACCAAGATCTC	642838
1039	CACATCGAATGGCGTTGGGGTGA	AAAAATACTTTCAAAAAATGTTGA	TGACTATGATGCT	1098
642837	CAGATCCATGGCGTGCATGCGGA	AGAAATGTTTTGGGNAATCTCTCG	TAGATGCTGATCCA	642778
1099	GCCAAATAATATCGGTGGCTG	GCATGGGCTGCTTCAACAGAACGG	ACGCTGTCCTTAT	1158
642777	GCTTCTAATGCTTTCACTGGCA	ATGGGCTGCGGGTAGCGGATGAC	CGCTTCGCCTTAT	642718
1159	TTTGGATTTTTTAATCCAAT	TATCCAGTCAAAAAAATTTTGAT	AATGACGGCCATGTCATC	1218
642717	TTCCGTATTTTTTAATCCGGT	CACCAACGGA	AAAAATTTTGATCCAGATGA	642658
1219	AAAAAATATGTTCCAGAA	1236		
642657	CGTCGCTGGGTACCGGAA	642640		

RESULT 15
US-09-938-842A-479
; Sequence 479, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME. AND METHODS OF USE

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; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 479
; LENGTH: 1839
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-479

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Query Match	7.3%;	Score 104.2;	DB 3;	Length 1839;
Best Local Similarity	48.9%;	Pred. No. 1.6e-14;		
Matches 280;	Conservative	0;	Mismatches 293;	Indels 0; Gaps 0;
Qy	774	AAGTAAGAACCTTCAAAAAGAAATAGCTTCGGCGAGCTTTTACAAATATGATCTATAG	833	
Db	846	AAGTGCAGATCTTTTCTTATAGGGAATCGGTTTAAGAGAGATTCTCGGTATATATATGTTT	905	
Qy	834	TGCCTTTCCACAACAAAAGAGGAAGCTATTCAAGAAAAAATTTTCGTTATATTTCATATG	893	
Db	906	CAACTTCCCGTTTACTACAGGCNAATCGTTGTTGAGTCATCTTCGGTTTTCCCTTGGGA	965	
Qy	894	AAATGACCCAGAAATGTTTGTCAAGTCGGCAAAAAGGGGAGACGGGGTACCCCTATATTTGA	953	
Db	966	TGCTGATGTTTGATAAGTTCAAGGCGCTGGAGACAAGGCGAGGACCGGTTATCGGTTGGTGA	1029	
Qy	954	TGCGCGAATCGGACAACCTGAAATCAAACCTGGTTGGATCGCACAATCGCTTAGAAGTATTAC	1013	
Db	1026	TGCGGGAATGAGAGAGCTTTTGGGCTACCGGATGGATGCATAACAGAAATAGAGTGATTGT	1085	
Qy	1014	TGCTCTCTTTTAGTTAAAAATTTACACATCGATTTCGGTTCGGGGTCGAAAAATCACTTTCA	1073	
Db	1086	TTCAAGCTTTTCTGCTGAAAGTTTCTTCTCTCCATCGAAATGGGGAATGAGTATTTCTG	1145	

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Qy 1074 AAAAATGTTGATTGACTATGATGCTGCCAATAATATCGTGGCTGGCAATGGGCTGCTTC 1133
Db 1146 GGATACACTTTTGGATGCTGATTTGGAAATGTGACATCCTTGGCTGGCAGTATATCTCTGG 1205
Qy 1134 AACAGGAACGGACGCTGTCCCTTATTTTCGGATTTTAAATCCAATTTATCCAGTCAAAAAA 1193
Db 1206 GAGTATCCCGATGGCCACGAGCTTGATCGCTTGGACAATCCCGGTTTACAAGGCGCAA 1265
Qy 1194 ATTTGATAATGACGGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCCACA 1253
Db 1266 ATATGACCCAGAAGGTGAGTACATAAAGCAATGGCTTCCCGAGCTTGCAGATTGCCAAC 1325
Qy 1254 AAAGTATATTCATCAACCAATCTAAATGAACGAAGCCTTACAAACGCAATATCATGTACA 1313
Db 1326 TGAATGGATCCATCATCCATGGGAGGCTCTTTAACCGTACTCAAGCTTCTGGTGTGGA 1385
Qy 1314 TTTAGGAGAAAATTATCCAAAACCCATTGTGGA 1346
Db 1386 ACTCGRACAAACTATGCGAACCCTTTGTAGA 1418
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Job time : 1294 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 20, 2005, 17:53:57 ; Search time 220 Seconds

(without alignments)
3195.076 Million cell updates/sec

Title: US-10-758-979-2

Perfect score: 1434

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

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- 2: /cgn2_6/prodata/1/pubnpa/US06_NEW_PUB.seq.*
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- 5: /cgn2_6/prodata/1/pubnpa/US09_NEW_PUB.seq.*
- 6: /cgn2_6/prodata/1/pubnpa/US10_NEW_PUB.seq.*
- 7: /cgn2_6/prodata/1/pubnpa/US11_NEW_PUB.seq.*
- 8: /cgn2_6/prodata/1/pubnpa/US12_NEW_PUB.seq.*
- 9: /cgn2_6/prodata/1/pubnpa/US13_NEW_PUB.seq.*
- 10: /cgn2_6/prodata/1/pubnpa/US14_NEW_PUB.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52.8	3.7	1296	US-10-467-657-1889	Sequence 1889, Ap
2	52.8	3.7	1296	US-10-467-657-6127	Sequence 6127, Ap
C 3	43.6	3.0	156544	US-11-121-086-81	Sequence 81, Appl
C 4	39.6	2.8	1082144	US-11-117-187-211	Sequence 211, App
C 5	39.4	2.7	900	US-10-750-185-37504	Sequence 37504, A
C 6	37.6	2.6	3001	US-11-145-703-181	Sequence 181, App
C 7	37.6	2.6	3001	US-11-145-703-197	Sequence 197, App
C 8	37.6	2.6	161874	US-11-121-086-75	Sequence 75, Appl
C 9	37.2	2.6	649	US-10-750-185-27667	Sequence 27667, A
C 10	37.2	2.6	1947	US-10-750-185-51012	Sequence 51012, A
C 11	37.2	2.6	207835	US-11-121-086-39	Sequence 39, Appl
C 12	37.2	2.6	207835	US-11-121-086-40	Sequence 40, Appl
C 13	37.2	2.6	398287	US-10-995-561-13396	Sequence 13396, A
C 14	36.4	2.5	7943	US-10-995-561-13397	Sequence 13397, A
C 15	36.2	2.5	1227	US-10-750-185-45849	Sequence 45849, A
C 16	36	2.5	965	US-10-750-185-63340	Sequence 63340, A
C 17	36	2.5	110950	US-10-857-780-2	Sequence 2, Appli
C 18	35.6	2.5	611587	US-11-117-187-209	Sequence 209, App
C 19	35.4	2.5	2982	US-10-793-626-4028	Sequence 4028, Ap
C 20	35.4	2.5	3114	US-10-750-185-32681	Sequence 32681, A
C 21	35.4	2.5	142303	US-11-121-086-42	Sequence 42, Appl
C 22	35	2.4	1839	US-10-750-185-59311	Sequence 59311, A
C 23	35	2.4	134174	US-11-121-086-99	Sequence 99, Appl

C	24	34.8	2.4	1069	6	US-10-750-185-27770	Sequence 27770, A
	25	34.6	2.4	3543	6	US-10-793-626-3493	Sequence 3493, Ap
	26	34.6	2.4	193084	7	US-11-121-086-82	Sequence 82, Appl
	27	34.6	2.4	398287	6	US-10-995-561-13396	Sequence 13396, A
	28	34.6	2.4	611587	7	US-11-117-187-209	Sequence 209, App
C	29	34.4	2.4	926	6	US-10-750-185-60151	Sequence 60151, A
	30	34.4	2.4	1544	6	US-10-750-185-37654	Sequence 37654, A
C	31	34.4	2.4	3649	6	US-10-793-626-3725	Sequence 3725, Ap
	32	34.2	2.4	964	6	US-10-750-185-57739	Sequence 57739, A
C	33	34.2	2.4	1184	6	US-10-750-185-42797	Sequence 42797, A
	34	34.2	2.4	1794	6	US-10-750-185-32037	Sequence 32037, A
C	35	34.2	2.4	2017	6	US-10-750-185-37628	Sequence 37628, A
	36	34	2.4	3159	6	US-10-793-626-4112	Sequence 4112, Ap
	37	34	2.4	139054	7	US-11-121-086-96	Sequence 96, Appl
C	38	33.8	2.4	1011	6	US-10-750-185-26282	Sequence 26282, A
	39	33.8	2.4	1695	6	US-10-750-185-33604	Sequence 33604, A
C	40	33.6	2.3	2269	6	US-10-750-185-38234	Sequence 38234, A
	41	33.6	2.3	2690	6	US-10-750-185-57602	Sequence 57602, A
C	42	33.6	2.3	5855	7	US-11-108-528-27	Sequence 27, Appl
	43	33.6	2.3	12462	6	US-10-995-561-13395	Sequence 13395, A
C	44	33.6	2.3	65931	6	US-10-995-561-13254	Sequence 13254, A
	45	33.4	2.3	1508	7	US-11-086-904-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-467-657-1889
; Sequence 1889, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1889
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1889

Query Match	3.7%	Score 52.8	DB 6	Length 1296
Best Local Similarity	52.8%	Pred. No. 0.00045		
Matches 114	Conservative 0	Mismatches 102	Indels 0	Gaps 0
QY	919	TGGCAAAAGGGGAGACGGGCTACCTATAATTCATGCGCAATGCGCAACTGAATCAA	978	
DB	904	TGGCAGCAGGCGCGGACCGGCATTCGGATTATCGATGCGCGATGCGCTTTTGCAAAA	963	
QY	979	ACTGGTTGGATGCAAAATCGCTTAAGAATGATTACTGCCTCTTTTTHAGTTAAAAATTTA	1038	
DB	964	ACCGCAGCTCCACCCGCCCTGAGCGCTTGAGCGCGGATTTTTCTGCCACGTTTTTA	1023	
QY	1039	CACATCGATTGGCGTTGGGGTGAAAATACCTTCAAAAATGTTGATTGACTATGATGCT	1098	
DB	1024	AACCTCCCGCCCGGAAGCGGAGATATGTTTTCGCCGAGCTGCTCA	1134	
QY	1099	GCCATAATATCGGTGGCTGGCAATGGGCTGCTTCA	1134	
DB	1084	GAATCAACCAAGCAACTGGCGGCTTGCCGCTCA	1119	

RESULT 2


```
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 37504
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Bovine 19866881386126
US-10-750-185-37504

Query Match      2.7%; Score 39.4; DB 6; Length 900;
Best Local Similarity 59.3%; Pred. No. 1;
Matches 67; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 772 TTAAGTAAAGAACTTCACAAAAGAAATTAGCTTGGCGGACTTTTACAAATATGATCTAT 831
Db 762 TCAGTAGGGAACCTCCAAAACATCTAGCTTTTATGCTCTTTTACTTTACGCCCTG 821

QY 832 AGTGGCTTCCACACAAAAGAGGAGCTATTCAGAAAAAATTTGCTTATAT 884
Db 822 TGTTGTTTCCCATGATAGTGGCAAAACCTTTTGCAAAAGACTCTTTTAAAT 874
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RESULT 6
US-11-145-703-181/c
; Sequence 181, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: 53.US16.DIV
; CURRENT APPLICATION NUMBER: US/11/145,703
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US/10/147,603
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 09/539,333
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 234
; SOFTWARE: Patent.pm
; SEQ ID NO 181
; LENGTH: 3001
; TYPE: DNA
; ORGANISM: Homo Sapiens
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; FEATURE:
; NAME/KEY: allele
; LOCATION: 1501
; OTHER INFORMATION: 99-25869-182 : polymorphic base A or C
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1482..1500
; OTHER INFORMATION: 99-25869-182.mis1
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: 1502..1521
; OTHER INFORMATION: 99-25869-182.mis2, complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1320..1340
; OTHER INFORMATION: upstream amplification primer
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1849..1868
; OTHER INFORMATION: downstream amplification primer, complement
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: 1489..1513
; OTHER INFORMATION: 99-25869-182 probe
US-11-145-703-181

Query Match      2.6%; Score 37.6; DB 7; Length 3001;
Best Local Similarity 51.8%; Pred. No. 4.9;
Matches 85; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1226 ATGTTCCAGAACTTAAGCAAGTGCCACAAAAGTATATTCATCAACCAATCTAATGAACG 1285
Db 1542 ATTTTACAGAAATGATGGTGATATTTAAACACATAATAATKTAACATTTATGCTAAAT 1483

QY 1286 AGCCCTTACAAACGCAATATCATGTACATTTAGGAGAAATTTATCCAAAACCCATTGTG 1345
Db 1482 GATTTTAATAAAGTTAATAATAATAATAAATAAAGAGAAATGATTATGACCCCAATTAAT 1423

QY 1346 ATTATGCATCAAGTAAAAACAAACATTTGTTCTATATGAACG 1389
Db 1422 AGTGTAGATCATGTAAAAAGAACTGTTTATGTCTACTAGAG 1379
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```
RESULT 7
US-11-145-703-197/c
; Sequence 197, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: 53.US16.DIV
; CURRENT APPLICATION NUMBER: US/11/145,703
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US/10/147,603
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 09/539,333
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
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; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 234
; SOFTWARE: Patent.pm
; SEQ ID NO 197
; LENGTH: 3001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1501
; OTHER INFORMATION: 99-26233-275 : polymorphic base T or C
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1502..1521
; OTHER INFORMATION: 99-26233-275.misl, complement
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1482..1500
; OTHER INFORMATION: 99-26233-275.mis2
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1755..1775
; OTHER INFORMATION: upstream amplification primer, complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1254..1274
; OTHER INFORMATION: downstream amplification primer
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1489..1513
; OTHER INFORMATION: 99-26233-275 probe
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 116
; OTHER INFORMATION: n=a, g, c or t
US-11-145-703-197

Query Match      2.6%; Score 37.6; DB 7; Length 3001;
Best Local Similarity 51.8%; Pred. No. 4.9;
Matches 85; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 1226 ATGTTCCAGAACTTAAGCAAGTGCACAAAGATATATTCATCAACCAAAATCTAATGAACG 1285
Db 1725 ATTTACAGAAATGATGGTGTATATTTAAACACATATAATGTAACATTTATGCTAAATT 1666

Qy 1286 AAGCCTTACAAACGCAATATCATGATTTAGGAGAAAATATCCAAAACCCATTGTGCG 1345
Db 1665 GATTTAATAAAGTTAATATAAATAATAACTAAGAGAAAATGATTATGACCAATTAAT 1606

Qy 1346 ATTATGCATCAAGTAAATAAACAACATGTTTCTATATGAGCG 1389
Db 1605 AGTGTAGATCATGTAAAAAAGAAGTGTTTTATGTTCTACCTAGAG 1562

RESULT 8
US-11-121-086-75/c
; Sequence 75, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138-6000-0000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
```

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75
; LENGTH: 161874
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-75

Query Match      2.6%; Score 37.6; DB 7; Length 161874;
Best Local Similarity 57.8%; Pred. No. 29;
Matches 67; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 1313 ATTTAGGAGAAAATTTATCCAAAACCCATTGTCGATTATGATCAAGTAAAAAACAACAT 1372
Db 49053 ATGAAGATGAATGTATAAAAATTTCTTGAATGATTATGATATCGTCAGAAACAATCC 48994

Qy 1373 TGTTCCTATATGAAGCAGCAAGAAATTCATCAAGAAATGAACAATCCAAAGTTT 1428
Db 48993 TAATGGAATAATGCAGAACTTTAAGAAGGTTCTTCAACAATGAAGAAATGATT 48938

RESULT 9
US-10-750-185-27667/c
; Sequence 27667, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27667
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-27667

Query Match      2.6%; Score 37.2; DB 6; Length 649;
Best Local Similarity 53.4%; Pred. No. 3.2;
Matches 78; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 102 ATTCCAAATGAATCCTCAACAATTTATTCAAGAAAGTGCTAATCATCAACGCTTTTTTTCG 161
Db 646 ATCATTATTGCTCTTTCTAGATTTTATATAAAGGAATCACTCAGTATACATATCTTTT 587

Qy 162 AAGCTTAGCTCGTTCAGAAAGCAATCGATCAAGAGGACATTTTACAAATCATGGTCGG 221
Db 586 ATGTCTAGCATCTCTCAGTTAGCATATGATGATTTTGAACATCTTTCTTATGCTGCTAG 527

Qy 222 CGAACCATTAGATTTATTTTTCAGGTT 247
Db 526 TGTTCATTAGTTTCTTTTCCAGTT 501

RESULT 10
US-10-750-185-51012
; Sequence 51012, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
```



```

; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 51012
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Bovine 19866881060052
US-10-750-185-51012

Query Match      2.6%; Score 37.2; DB 6; Length 1947;
Best Local Similarity 47.1%; Pred. No. 5.2;
Matches 114; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

Qy 1149 TGTCCCTTTATTCGGATTTTAAATCCAAATTCAGTCACAAATAATTTGATATGACGG 1208
Db 1564 TTTGCTTTTACAAAGAAATAGCAATTTAGTGTTTAGAGTAAATGAATACCTTTTGTACTT 1623

Qy 1209 CCAGTTCAATCAAAATATGTTCCAGAACTTAAGCAAGTGCACAAAAGTATATTCATCA 1268
Db 1624 ACTGTGCTGATGAAGAAATAGGAAAGAAAGAAACCAATTAATTAATATATATAAAA 1683

Qy 1269 ACCAAATCTAATGAACGAGCCTTACAAACGCAATATCATGTACATTTAGGAGAAATTA 1328
Db 1684 ACNAATCAAACTATATATATATATATATATATATATATATATATATATATATATATA 1743

Qy 1329 TCCAAACCCATTTGCGATTTATGCAATCAAGTAAAGTAAACAAACAAATGTTTCTATATGAAGC 1388
Db 1744 AATTGCTCATATGTCATTTATTTATTTATTTTCAATTAAGCCTCAITTTGGGAAAGATAA 1803

Qy 1389 GA 1390
Db 1804 GA 1805

RESULT 11
US-11-121-086-39/c
; Sequence 39, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 39
; LENGTH: 207835
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-39

Query Match      2.6%; Score 37.2; DB 7; Length 207835;
Best Local Similarity 47.1%; Pred. No. 40;
Matches 114; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

Qy 1171 AATCCAATTTATCCAGTCACAAATAATTTGATATATGACGCCAGTTCATCAAAAAATATGTT 1230
Db 185580 AAGCAAAATGCAATTAATAAACAAGATTAATAGCTGGACCCCAATTAACCTAAAGAGCTTTT 185521

Qy 1231 CCAGAACTTAAAGCAAGTGCACAAAGATATATTCATCAACCAAAATCTTAATGAACGAGCC 1290
Db 185520 GCATGGCAAAAGGAACAGTCAGCAAGTAAACAGACAAACCCACAGAGTGGGAGAAATCT 185461

Qy 1291 TTACAAACGCAATATCATGTATCATTTAGGAGAAATTTATCCAAACCCATTTGTCGATTAT 1350
Db 185460 TCACAATCTATACATCTGCACAAAGACTTAATAACAAGAAATCTGCAATGAACTCAAAACAA 185401

Qy 1351 GCATCAAGTAAACAAACAAATGTTTCTATATGAAGCGAGCAAAAGAAATTCATCAAGAA 1410
Db 185400 TCAGTAAGAAAAAACAACAATCCCAACCAAAAGAGTGGGTAGGACATGAATAGTCAA 185341

Qy 1411 AT 1412
Db 185340 TT 185339

RESULT 12
US-11-121-086-40/c
; Sequence 40, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 40
; LENGTH: 207835
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-40

Query Match      2.6%; Score 37.2; DB 7; Length 207835;
Best Local Similarity 47.1%; Pred. No. 40;
Matches 114; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

Qy 1171 AATCCAATTTATCCAGTCACAAATAATTTGATATATGACGCCAGTTCATCAAAAAATATGTT 1230
Db 185580 AAGCAAAATGCAATTAATAAACAAGATTAATAGCTGGACCCCAATTAACCTAAAGAGCTTTT 185521

Qy 1231 CCAGAACTTAAAGCAAGTGCACAAAGATATATTCATCAACCAAAATCTTAATGAACGAGCC 1290
Db 185520 GCATGGCAAAAGGAACAGTCAGCAAGTAAACAGACAAACCCACAGAGTGGGAGAAATCT 185461

Qy 1291 TTACAAACGCAATATCATGTATCATTTAGGAGAAATTTATCCAAACCCATTTGTCGATTAT 1350
Db 185460 TCACAATCTATACATCTGCACAAAGACTTAATAACAAGAAATCTGCAATGAACTCAAAACAA 185401

Qy 1351 GCATCAAGTAAACAAACAAATGTTTCTATATGAAGCGAGCAAAAGAAATTCATCAAGAA 1410
Db 185400 TCAGTAAGAAAAAACAACAATCCCAACCAAAAGAGTGGGTAGGACATGAATAGTCAA 185341

Qy 1411 AT 1412
Db 185340 TT 185339

RESULT 13
US-10-995-561-13396/c
; Sequence 13396, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13396
; LENGTH: 398287
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(398287)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13396

Query Match          2.6%; Score 37.2; DB 6; Length 398287;
Best Local Similarity 47.1%; Pred. No. 53;
Matches 114; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

Qy 1191 AAAATTTGATATGACGGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCC 1250
Db 51285 AAAATTGACAAATGGGCTCCAGTTAAACTAAAGAGCTTCTGCACAGCAAAAAGGAATATC 51226

Qy 1251 ACAAAGTATATTCATCAACCAATCTTAATGAACGAAGCCCTTACAAACGCAATATCATGT 1310
Db 51225 ACCAGAGTGACAGGCAACCTTACAGAATGGGAGAAAAATTTTGCATCTTATCCATCTGAC 51166

Qy 1311 ACATTTAGGAGAAAATTTATCCAAAACCCATTGTCGATTATGCATCAAGTAAAAACAAAC 1370
Db 51165 AAAGGGCTAATATCCAGATCTACAGAAATTTAAACAAATTTACAAGAAAAAAAACAG 51106

Qy 1371 ATGTTTCTATATGAAGCGAGCAAGAAATTCATCAAGAATGAACAATCCAAGTTTCA 1430
Db 51105 ACAACTCCATCAAAAAGTAGTGAAGGATATGAACAGCAATTTATCAAAAGNAGACATTT 51046

Qy 1431 AT 1432
Db 51045 AT 51044

RESULT 14
US-10-995-561-13397/c
; Sequence 13397, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13397
; LENGTH: 7943
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13397

Query Match          2.5%; Score 36.4; DB 6; Length 7943;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 91; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 1190 AAAAATTTGATATGACGGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCC 1249
Db 4024 AAAAACTGACAAATGGGATCTTAATTAACCTAAAGAGCTTCTGCACAGCAAAAAGGAATAT 3965

Qy 1250 CAAAAAGTATATTCATCAACCAATCTTAATGAACGAAGCCCTTACAAACGCAATATCATG 1309
Db 3964 CAGCAGAGTAAAGAGATAACCTACAGATGGGAGAAAATATTATCAAACTATGTATCTCA 3905

Qy 1310 TACATTTAGGAGAAAAATTTATCCAAAAACCCATGTCGATTATGTCATCAAGTAAAAACAAA 1369
Db 3904 CAAAGGCTTAATATCCAGAACTTATAGGAATTTAAACACATGTACAAAGCAAAAAACAAA 3845

Qy 1370 CA 1371
```

```
Db 3844 CA 3843

RESULT 15
US-10-750-185-45849/c
; Sequence 45849, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45849
; LENGTH: 1227
; TYPE: DNA
; ORGANISM: Bovine 19866881281641
US-10-750-185-45849

Query Match          2.5%; Score 36.2; DB 6; Length 1227;
Best Local Similarity 48.3%; Pred. No. 7.6;
Matches 101; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

Qy 1071 TCAAAAAATGTTGATTGCACTATGCTGCCAATAATATCGTGGCTGGCAATGGGCTGC 1130
Db 281 TCAATGTAACCAACATCATCATATTACTATAATAAATTTAAATTTAAGATAACATTC 222

Qy 1131 TTCAACAGGAACGGACGCTGTCCTTATTTTCGGATTTTAAATCCAAATTTATCCAGTCAAA 1190
Db 221 TCCCATATGCTTGAATTTTCTCTTATTCTTAAATTTTGAACCTTTTATGACAGTTA 162

Qy 1191 AAAATTTGATATGACGGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCC 1250
Db 161 ACAGTGTGAAACTACAAACATTCCTCCAGTAAAGATACACAAACATACCCACTTAAT 102

Qy 1251 AAAAAAGTATATTCATCAACCAAACTAA 1279
Db 101 TCAAGGCATGATACCTAGATATCAAA 73

Search completed: December 20, 2005, 22:14:16
Job time : 224 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 20, 2005, 14:07:11 : Search time 944 Seconds
(without alignments)
10124.120 Million cell updates/sec

Title: US-10-758-979-2
Perfect score: 1434
Sequence: 1 atgaagagagaatatggtt.....acaatccaaggtttcaataa 1434

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
7: geneseqn2002bs.*
8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004as.*
13: geneseqn2004bs.*
14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1434	100.0	1434	ADJ33289	Adj33289 Enterococ
2	1434	100.0	2267	ADJ33288	Adj33288 Enterococ
3	1432.8	99.9	5277	AAJ13199	Aax13199 Enterococ
4	1432.8	99.9	5277	ABS98994	Abx98994 Enterococ
5	942	65.7	966	ADH83427	Adh83427 Enterococ
6	597	41.6	609	ADH83428	Adh83428 Enterococ
7	526.4	36.7	2460	ABQ70791	Abq70791 Listeria
8	518.4	36.2	110000	ABQ69245_06	Continuation (7 of
9	518.4	36.2	110000	ABQ67197_05	Continuation (6 of
10	516.8	36.0	110000	ABA03041_06	Continuation (7 of
11	416.8	29.1	1451	ABQ68877	Abq68877 Listeria
12	396.2	27.6	1440	ABN70089	Abn70089 Streptoco
13	212.2	14.8	1446	ADF03864	Adf03864 Bacterial
14	206.2	14.4	1389	ACF74095	Acf74095 Staphyloc
15	206.2	14.4	1393	AAV74905	Aav74905 Staphyloc
16	203.4	14.2	1608	ADA29102	Ada29102 DNA encod
17	201.4	14.0	5024	AAQ55139	Aaq55139 Staphyloc
18	201.4	14.0	5024	ABZ77355	Abz77355 Nucleotid
19	201.4	14.0	5024	AAI51843	Aai51843 Staphyloc

20	199	13.9	1380	6	ABN93166	Abn93166 Staphyloc	
21	199	13.9	1380	13	ADS04064	Ads04064 Staphyloc	
22	184.8	12.9	110000	6	ABA92787_3	Continuation (4 of	
c	23	157.8	11.0	110000	14	AE339175_02	Continuation (3 of
c	24	157.8	11.0	110000	14	AE339175_03	Continuation (4 of
c	25	157.8	11.0	194588	14	AE335717	Aeb35717 L. pneumo
c	26	156.4	10.9	184951	14	AE342739	Aeb42739 L. pneumo
c	27	156.4	10.9	185021	14	AE339169	Aeb39169 L. pneumo
c	28	154.6	10.8	110000	14	AE342739_02	Continuation (3 of
c	29	117.4	8.2	1248	11	ABD00369	Abd00369 Klebsiell
30	114.8	8.0	1404	5	AAH65666	Aah65666 C. glutami	
31	114.8	8.0	1428	8	ACA00095	Aca00095 C. glutami	
c	32	114.8	8.0	349980	5	AAH68525	Aah68525 C. glutami
c	33	114.8	8.0	349980	5	AAH68526	Aah68526 C. glutami
c	34	109.8	7.7	1638	11	ABD15391	Abd15391 Pseudomon
c	35	109.8	7.7	2514	11	ABD15538	Abd15538 Pseudomon
36	104.2	7.3	978	3	AAC37888	Aac37888 Arabidops	
37	104.2	7.3	1839	3	AAC48461	Aac48461 Arabidops	
38	104.2	7.3	1839	6	ABZ12674	Abz12674 Arabidops	
39	104.2	7.3	2188	3	AAC37009	Aac37009 Arabidops	
40	102.6	7.2	2200	2	AAT16309	Aat16309 Arabidops	
41	101.6	7.1	535	8	ABZ56081	Abz56081 Aspergill	
42	99.2	6.9	1883	13	ADX11011	Adx11011 Plant ful	
43	99.2	6.9	2264	13	ADX36310	Adx36310 Plant ful	
44	99.2	6.9	2533	13	ADX64757	Adx64757 Plant ful	
45	99.2	6.9	2649	13	ADX49572	Adx49572 Plant ful	

ALIGNMENTS

RESULT 1
ADJ33289
ID ADJ33289 standard; DNA; 1434 BP.
XX
XX ADJ33289;
AC
XX
DT 22-APR-2004 (first entry)
XX
DE Enterococcus faecalis photolase encoding DNA SEQ ID NO:2.
XX
KW Enterococcal; virulence factor; drug discovery; vaccine;
KW microbial infection; antimicrobial; bacterial pathogenesis; photolase;
KW enzyme; gene; ds.
XX
OS Enterococcus faecalis.
XX
FH Key Location/Qualifiers
FT CDS 1..1434
FT /*tag= a
FT /product= "photolase"
XX
XX WO2003056295-A2.
XX
XX 10-JUL-2003.
XX
XX 18-JUL-2002; 2002WO-US022979.
XX
XX 18-JUL-2001; 2001US-0306212P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX
XX Ausubel FM, Garsin D, Mylonakis EE, Calderwood SB, Sifri CD;
XX WPI; 2003-559298/52.
XX P-PSDB; ADJ33243.
XX
XX New polypeptide, useful for preparing a composition for treating or
XX preventing a microbial infection.
XX
XX Claim 2; SEQ ID NO 2; 140pp; English.
XX
XX The present invention describes Enterococcal virulence factors (1), which

CC can act as targets for drug discovery. Also described: (1) an isolated
CC nucleic acid encoding (I); (2) a vector or host cell comprising the
CC nucleic acid; (3) a method of screening a compound for effectiveness as
CC an antagonist of (I); (4) a composition comprising the antagonist
CC compound; (5) a method of screening a compound for effectiveness in
CC altering expression of (I); (6) a method of treating an individual;
CC vaccine composition comprising the polypeptide and a vehicle; and (8) a
CC method of treating or preventing a microbial infection. (I) is useful for
CC preparing a composition having antimicrobial activity for treating or
CC preventing a bacterial pathogenesis e.g. microbial infection. The present
CC sequence encodes an Enterococcal photolysase, which is used in the
CC exemplification of the present invention.

XX
SQ Sequence 1434 BP; 496 A; 261 C; 269 G; 408 T; 0 U; 0 Other;

Query Match 100.0%; Score 1434; DB 10; Length 1434;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAGAAGTAATGGTTAGACGGTATTACGATTACAGGATTAAGCAATTAAGCA 60
Db 1 ATGAAGAAGTAATGGTTAGACGGTATTACGATTACAGGATTAAGCAATTAAGCA 60
Qy 61 CACGGCTTACAAAATCTCGACGCTGATGAATGGATTTATTTCCAAATGAATCCTCAA 120
Db 61 CACGGCTTACAAAATCTCGACGCTGATGAATGGATTTATTTCCAAATGAATCCTCAA 120
Qy 121 CAATTTATTCAGAAAGTGCTAATACAGCTTTTTTTTGAAGCTTAGCTCGTTCAAA 180
Db 121 CAATTTATTCAGAAAGTGCTAATACAGCTTTTTTTTGAAGCTTAGCTCGTTCAAA 180
Qy 181 GAACGAATCGATCAAGAGGCAATTTACAAATCATGTCGGCGAACCATTAGATTATTT 240
Db 181 GAACGAATCGATCAAGAGGCAATTTACAAATCATGTCGGCGAACCATTAGATTATTT 240
Qy 241 TCAGCTTTGAACCGCAATATCCCGATTGGCAGGCCATTTATTTTAATGAAGTACTTGT 300
Db 241 TCAGCTTTGAACCGCAATATCCCGATTGGCAGGCCATTTATTTTAATGAAGTACTTGT 300
Qy 301 GGCTTTGGGGCAAGCGGGACAGCAAGCTATGCGCTTTTTTGAAGAAATAATATTTCAG 360
Db 301 GGCTTTGGGGCAAGCGGGACAGCAAGCTATGCGCTTTTTTGAAGAAATAATATTTCAG 360
Qy 361 TCTTTCTCTTTCAAGATGCTATTTTCGATGGCTCTCAAGAAATTAAGAGACGATGCG 420
Db 361 TCTTTCTCTTTCAAGATGCTATTTTCGATGGCTCTCAAGAAATTAAGAGACGATGCG 420
Qy 421 AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAATGGAAGAGCGCCCTAAAGAAACA 480
Db 421 AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAATGGAAGAGCGCCCTAAAGAAACA 480
Qy 481 CCGATTCTGTTTCTTATACAGCTGAAATAATTTTAGTGGTGTCTTTTTCCAGAAGAG 540
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Qy 541 GAACGAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAACACACTATAGTGTGCGGAA 600
Db 541 GAACGAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAACACACTATAGTGTGCGGAA 600
Qy 601 GAAACAGCCAGAGCGCTTAAATACTTTATTCATCAAAAACCTTCAATCCTATGAAAT 660
Db 601 GAAACAGCCAGAGCGCTTAAATACTTTATTCATCAAAAACCTTCAATCCTATGAAAT 660
Qy 661 AAGCGTGATTTTCTTATACAGGATCAAAACGAGTCTGTCTACTTTTTTAAGAACGGGA 720
Db 661 AAGCGTGATTTTCTTATACAGGATCAAAACGAGTCTGTCTACTTTTTTAAGAACGGGA 720
Qy 721 GAACCTTCGATTCCGACCAATTTGCAAGAGCTTCATCTGTGCCTTCTAGCTTAAGTAAA 780
Db 721 GAACCTTCGATTCCGACCAATTTGCAAGAGCTTCATCTGTGCCTTCTAGCTTAAGTAAA 780
Qy 781 GAAACCTTCAAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCTATAGTGGCTTT 840
Db 781 GAAACCTTCAAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCTATAGTGGCTTT 840

Db 781 GAAACCTTCAAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCTATAGTGGCTTT 840
Qy 841 CCACACAAAAGAGAGAGCTATTCAAGAAAATTTTCGTATATTTCAATGGACAAATGAC 900
Db 841 CCACACAAAAGAGAGAGCTATTCAAGAAAATTTTCGTATATTTCAATGGACAAATGAC 900
Qy 901 CCAGAAATGTTTCTCAAGTGGCAAAAAGGGAGACGGGTACCTATAATTTGATGCGCA 960
Db 901 CCAGAAATGTTTCTCAAGTGGCAAAAAGGGAGACGGGTACCTATAATTTGATGCGCA 960
Qy 961 ATGCGCAATCGAATCAAACTGGTGGATGCAAAATCGCTTAAGAATGATTTACTGCTCT 1020
Db 961 ATGCGCAATCGAATCAAACTGGTGGATGCAAAATCGCTTAAGAATGATTTACTGCTCT 1020
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Db 1021 TTTTATGTTAAAAATTTTACACATCGATTGGCGTTGGGGTGAATAATCTTTCAAAAATG 1080
Qy 1081 TTGATTGACTATGATCTGCAATAATATCGGTGGCTGGCAATGGCTGCTTCAACAGGA 1140
Db 1081 TTGATTGACTATGATCTGCAATAATATCGGTGGCTGGCAATGGCTGCTTCAACAGGA 1140
Qy 1141 ACGGACGCTGCTCCCTTATTTTCGGATTTTAAATFCCAATTCAGATCAAAAAATTTGAT 1200
Db 1141 ACGGACGCTGCTCCCTTATTTTCGGATTTTAAATFCCAATTCAGATCAAAAAATTTGAT 1200
Qy 1201 AATGACGGCGAGTTTCAAAAAATATGTTCCAGAACTTAAGCAAGTGGCCACAAAAGTAT 1260
Db 1201 AATGACGGCGAGTTTCAAAAAATATGTTCCAGAACTTAAGCAAGTGGCCACAAAAGTAT 1260
Qy 1261 ATTCAATCAACCAATCTAATGAACGAAGCTTTACAAACGAATATCATGTACATTTAGGA 1320
Db 1261 ATTCAATCAACCAATCTAATGAACGAAGCTTTACAAACGAATATCATGTACATTTAGGA 1320
Qy 1321 GAAATTTATCCAAACCCATTTGCGATTATGCAATCAAGTAAAAAACAACATTTGTTCTA 1380
Db 1321 GAAATTTATCCAAACCCATTTGCGATTATGCAATCAAGTAAAAAACAACATTTGTTCTA 1380
Qy 1381 TATGAAGCGAGCAAGAAATTCATCAAGAAATGAACAATCCAAGTTTCAATAA 1434
Db 1381 TATGAAGCGAGCAAGAAATTCATCAAGAAATGAACAATCCAAGTTTCAATAA 1434

RESULT 2

ADJ33288
ID ADJ33288 standard; DNA; 2267 BP.

XX AC ADJ33288;

XX AC (first entry)

XX 22-APR-2004 (first entry)

XX Enterococcus faecalis photolysase encoding DNA SEQ ID NO:1.

DE DE Enterococcal; virulence factor; drug discovery; vaccine;

XX KW microbial infection; antimicrobial; bacterial pathogenesis; photolysase;

XX KW enzyme; gene; ds.

XX OS Enterococcus faecalis.

XX Key Location/Qualifiers

XX CDS 568..2001

XX FT /*tag= a

XX FT /product= "photolysase"

XX WO2003056295-A2.

XX 10-JUL-2003.

XX 18-JUL-2002; 2002WO-US022979.

XX 18-JUL-2001; 2001US-0306212P.

XX (GEHO) GEN HOSPITAL CORP.

XX Ausubel FM, Garain D, Mylonakis EE, Calderwood SB, Sifri CD;
XX WPI; 2003-559298/52.
XX P-PSDB; ADJ33243.
XX New polypeptide, useful for preparing a composition for treating or
XX preventing a microbial infection.
XX Disclosure; SEQ ID NO 1; 140pp; English.
XX The present invention describes Enterococcal virulence factors (I), which
XX can act as targets for drug discovery. Also described: (1) an isolated
XX nucleic acid encoding (I); (2) a vector or host cell comprising the
XX nucleic acid; (3) a method of screening a compound for effectiveness as
XX an antagonist of (I); (4) a composition comprising the antagonist
XX compound; (5) a method of screening a compound for effectiveness in
XX altering expression of (I); (6) a method of treating an individual;
XX vaccine comprising the polypeptide and a vehicle; and (8) a
XX method of treating or preventing a microbial infection. (I) is useful for
XX preparing a composition having antimicrobial activity for treating or
XX preventing a bacterial pathogenesis e.g. microbial infection. The present
XX sequence encodes an Enterococcal photolase, which is used in the
XX exemplification of the present invention.
SQ Sequence 2267 BP; 801 A; 387 C; 416 G; 663 T; 0 U; 0 Other;
Query Match 100.0%; Score 1434; DB 10; Length 2267;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAAGAGTAAATGTTTGTAGCGTGATTTACGATTACAGGATAATAAGCATTAGCA 60
DB 568 ATGAAAGAGTAAATGTTTGTAGCGTGATTTACGATTACAGGATAATAAGCATTAGCA 627
QY 61 CACGGGTACAAAATCTGCAGCTGATGATTTATTTATTTCCAAATGAATCCTCAA 120
DB 628 CACGGGTACAAAATCTGCAGCTGATGATTTATTTATTTCCAAATGAATCCTCAA 687
QY 121 CAATTTATTTCAAGAAAGTCTTAATCAACGCTTTTTTGGCAAGCTTAGCCCTCGTTCAA 180
DB 688 CAATTTATTTCAAGAAAGTCTTAATCAACGCTTTTTTGGCAAGCTTAGCCCTCGTTCAA 747
QY 181 GAACGAATCGATCAAGAGGCACATTTACAAATCATGGTCGGCGAACCATTAGATTTATTT 240
DB 748 GAACGAATCGATCAAGAGGCACATTTACAAATCATGGTCGGCGAACCATTAGATTTATTT 807
QY 241 TCACGTTTGAACGCAAAATTCACGATTCGGAGCCATTTATTTAATGAAGATCTTGT 300
DB 808 TCACGTTTGAACGCAAAATTCACGATTCGGAGCCATTTATTTAATGAAGATCTTGT 867
QY 301 GCGTTTGGGCAAGCGGACCAAGCAAGCTATGCGCTTTTTTGAAGAAATAATATTCAAG 360
DB 868 GCGTTTGGGCAAGCGGACCAAGCAAGCTATGCGCTTTTTTGAAGAAATAATATTCAAG 927
QY 361 TCTTTCTCTTTTCAAGATGCTATTTTGCATGGCTTGAAGAAATAATGAAGAACGATGCG 420
DB 928 TCTTTCTCTTTTCAAGATGCTATTTTGCATGGCTTGAAGAAATAATGAAGAACGATGCG 987
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DB 988 AGCAAGTACCAAGTGTGTAGCCCTATTACAAATAATGAAGAGCGCGCTTAAGAAACA 1047
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DB 1048 CCGATTCCTGTTTCCCTATACAGCTGAAAAATTTTTAGTGCCTGCTTTTTTCCAGAAAGAG 1107
QY 541 GAAGCAGCTTTATCGTGAACAGATTTGGAGGATTTCTTTTAAACACATATATGTCGCGGAA 600
DB 1108 GAAGCAGCTTTATCGTGAACAGATTTGGAGGATTTCTTTTAAACACATATATGTCGCGGAA 1167
QY 601 GAAACAGCCAGAGGCGCTTAAATACATTTTATTTGATCAAAAACCTCAATCCTATGAAAT 660

DB 1168 GAAACAGCCAGAGGCGCTTAAATACATTTTATTTGATCAAAAACCTTCAATCCTATGAAAT 1227
QY 661 AAGCGTGATTTTCTTATCAGGATCAAAACGAGTCATCTGTCTACTTTTTTAAAGAACGGGA 720
DB 1228 AAGCGTGATTTTCTTATCAGGATCAAAACGAGTCATCTGTCTACTTTTTTAAAGAACGGGA 1287
QY 721 GAACCTTTTCGATTCGACCATTTTGGCAAGAGCTTGTGCTCTGTGCTTCTAGCTTAAAGTAAA 780
DB 1288 GAACCTTTTCGATTCGACCATTTTGGCAAGAGCTTGTGCTCTGTGCTTCTAGCTTAAAGTAAA 1347
QY 781 GAAACCTTTCAAAAAGAAATTTAGCTTGGCGGACATTTTACAAATATGATCTATAGTGGCTTT 840
DB 1348 GAAACCTTTCAAAAAGAAATTTAGCTTGGCGGACATTTTACAAATATGATCTATAGTGGCTTT 1407
QY 841 CCACAAACAAAAGAGGAGGCTATTTCAGAAAAATTTTCGTTATATTCAATGACACAAATGAC 900
DB 1408 CCACAAACAAAAGAGGAGGCTATTTCAGAAAAATTTTCGTTATATTCAATGACACAAATGAC 1467
QY 901 CCAGAAATGTTTTCAGAGTGGCAAAAAGGGGAGACGGGTACCTATAATTTGATGGCGCA 960
DB 1468 CCAGAAATGTTTTCAGAGTGGCAAAAAGGGGAGACGGGTACCTATAATTTGATGGCGCA 1527
QY 961 ATGCGACAACTGAATCAAACTGTTGGATGCACAATCGCTTAAGAAATGATTTACTGCTCT 1020
DB 1528 ATGCGACAACTGAATCAAACTGTTGGATGCACAATCGCTTAAGAAATGATTTACTGCTCT 1587
QY 1021 TTTTGTAGTAAAAATTTACACATCGATTGGCGTTGGGGTGAAAAATATCTTTCAAAAATG 1080
DB 1588 TTTTGTAGTAAAAATTTACACATCGATTGGCGTTGGGGTGAAAAATATCTTTCAAAAATG 1647
QY 1081 TTGATTGACTATGATGCTGCCAATAATATCGTGGCTGGCAATGGGCTGCTTCAACAGGA 1140
DB 1648 TTGATTGACTATGATGCTGCCAATAATATCGTGGCTGGCAATGGGCTGCTTCAACAGGA 1707
QY 1141 ACGGACGCTGCTCTTATTTTCGGATTTTAAATCCAATATTCAGTCAAAAAATTTTGTAT 1200
DB 1708 ACGGACGCTGCTCTTATTTTCGGATTTTAAATCCAATATTCAGTCAAAAAATTTTGTAT 1767
QY 1201 AATGACGGCAGTTTCATCAAAAATATGTTCCAGAACTTAAGCAAGTGCACAAAAGTAT 1260
DB 1768 AATGACGGCAGTTTCATCAAAAATATGTTCCAGAACTTAAGCAAGTGCACAAAAGTAT 1827
QY 1261 ATTCAATCAACCAATCTAATCAAGCAAGCCTTTACAAACGCAATATCATGTATTTAGGA 1320
DB 1828 ATTCAATCAACCAATCTAATCAAGCAAGCCTTTACAAACGCAATATCATGTATTTAGGA 1887
QY 1321 GAAATTTATCCAAACCCATTTGCTGATTTATGATCAAGTAAACAAACATTTGTTCTA 1380
DB 1888 GAAATTTATCCAAACCCATTTGCTGATTTATGATCAAGTAAACAAACATTTGTTCTA 1947
QY 1381 TATGAGCGGACGCAAGAAATTTTCATCAAGAAATGACAAATCCAGGTTTCAATAA 1434
DB 1948 TATGAGCGGACGCAAGAAATTTTCATCAAGAAATGACAAATCCAGGTTTCAATAA 2001

RESULT 3
AA13199
ID AA13199 standard; DNA; 5277 BP.
XX
AC AA13199;
XX
DT 19-MAR-1999 (first entry)
XX
DE Enterococcus faecalis genome contig SEQ ID NO:262.
XX
KW Enterococcus faecalis; contig; detection; Enterococcal infection;
KW vaccine; attenuation; computer readable medium; ds.
XX
OS Enterococcus faecalis.
XX
PN WO980555-A2.
XX
PD 12-NOV-1998.

PA (BUSH/) BUSH D.
XX Doucette-Stamm LA, Bush D;
XX WPI; 2003-895394/82.
DR P-PSDB; ADH86833.
XX
XX New nucleic acid comprising a sequence encoding an Enterococcus faecalis
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating E. faecalis infection.
XX
XX Disclosure; SEQ ID NO 1313; 193pp; English.
XX
XX The invention relates to Enterococcus faecalis polynucleotides and
CC polypeptides. The invention also relates to a recombinant expression
CC vector comprising a polynucleotide operably linked to a transcription
CC regulatory element, a cell comprising a recombinant vector, a method for
CC producing an E. faecalis polypeptide, an isolated nucleic acid comprising
CC a sequence not given in the specification, a recombinant vector
CC comprising the nucleic acid and a cell comprising the recombinant vector.
CC The polynucleotides can be used to detect the presence of E. faecalis in
CC a sample. The sequences are useful for preparing a composition for
CC diagnosing or treating Enterococcus faecalis infection. This sequence
CC represents an E. faecalis polynucleotide of the invention.
XX
XX Sequence 609 BP; 225 A; 109 C; 111 G; 164 T; 0 U; 0 Other;
SQ

Query Match 41.6%; Score 597; DB 10; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.7e-139;
Matches 608; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 827 TCTATAGTCGGTTTCACACAAAAGAGGAGCTATTTCAGAAAAATTCGTTATATTC 886
DB 1 TCTATAGTCGGTTTCACACAAAAGAGGAGCTATTTCAGAAAAATTCGTTATATTC 60
QY 887 AATGACAAATGACCCAGAAATGTTGTCAAGTGGCAAAAGGGGAGAC-GGGGTACCCCT 945
DB 61 AATGACAAATGACCCAGAAATGTTGTCAAGTGGCAAAAGGGGAGACGGGGTACCCCT 120
QY 946 ATAATTGATCGCGCAATCGCACAACTGAATCAAACTGGTTGATGCACAATCGTTAAGA 1005
DB 121 ATAATTGATCGCGCAATCGCACAACTGAATCAAACTGGTTGATGCACAATCGTTAAGA 180
QY 1006 ATGATTACTGCTCTTTTGTAGTAAATTTACACATCGATTGGGTTGGGTCAGAAA 1065
DB 181 ATGATTACTGCTCTTTTGTAGTAAATTTACACATCGATTGGGTTGGGTCAGAAA 240
QY 1066 TACTTTCAAAAATGTTGATTGACATGATGCTGCAATAATATCGGTGGCTGGCAATGG 1125
DB 241 TACTTTCAAAAATGTTGATTGACATGATGCTGCAATAATATCGGTGGCTGGCAATGG 300
QY 1126 GCTGCTTCAACAGGAACGACGCTGTCCCTTATTTTCGGATTTTAAATCCAAATATCCAG 1185
DB 301 GCTGCTTCAACAGGAACGACGCTGTCCCTTATTTTCGGATTTTAAATCCAAATATCCAG 360
QY 1186 TCAAAAAATTTGATAATGACGGCGAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCA 1245
DB 361 TCAAAAAATTTGATAATGACGGCGAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCA 420
QY 1246 GTGCCCAAAAGTATATTCATCAACCAATCTAATGAACGAAGCCCTTACAAACGCAATAT 1305
DB 421 GTGCCCAAAAGTATATTCATCAACCAATCTAATGAACGAAGCCCTTACAAACGCAATAT 480
QY 1306 CATGTACATTTAGGAGAAAATATCCAAACCCATTTGTCGATTTATGTCATCAAGTAAAAA 1365
DB 481 CATGTACATTTAGGAGAAAATATCCAAACCCATTTGTCGATTTATGTCATCAAGTAAAAA 540
QY 1366 CAACATTTGTTCTATATGAAGCGAGCAAGAAATTCATCAGAAATGAACAAATCCAGG 1425
DB 541 CAACATTTGTTCTATATGAAGCGAGCAAGAAATTCATCAGAAATGAACAAATCCAGG 600
QY 1426 TTTCATAAA 1434
|||||

DB 601 TTTCATAAA 609
RESULT 7
ABQ070791
ID ABQ070791 standard; DNA; 2460 BP.
XX
XX AC ABQ070791;
XX 29-AUG-2003 (revised)
DT 29-AUG-2002 (first entry)
XX
XX Listeria monocytogenes 4b contig DNA sequence #733.
XX
XX Antibacterial; Listeria; food contamination; mutational analysis;
XX infection; ds.
XX
XX Listeria monocytogenes ATCC 19115.
XX
XX WO200228891-A2.
XX
XX 11-APR-2002.
XX
XX 04-OCT-2001; 2001WO-FR003061.
XX
XX 04-OCT-2000; 2000FR-00012697.
XX
XX (INSP) INST PASTEUR.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX
XX Kunst F, Glaser P;
XX
XX WPI; 2002-332479/37.
XX
XX New genomic sequences from Listeria species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators.
XX
XX Claim 14; SEQ ID NO 3604; 180pp; French.
XX
XX The present invention relates to nucleic acid sequences (AB067188-
CC ABQ71212) from Listeria sp. The sequences are useful as probes and
CC primers for identification and/or detection of Listeria (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of gene
CC expression. Proteins encoded by the nucleic acid sequences can be used to
CC screen for compounds that modulate gene expression, replication and
CC pathogenicity of Listeria (potential therapeutic agents), also for
CC treating infections by Listeria, and are useful as immunogens in anti-
CC Listeria vaccines. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated
CC on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 2460 BP; 774 A; 410 C; 564 G; 712 T; 0 U; 0 Other;
Query Match 36.7%; Score 526.4; DB 6; Length 2460;
Best Local Similarity 61.6%; Pred. No. 1.4e-121;
Matches 883; Conservative 0; Mismatches 536; Indels 15; Gaps 2;
QY 1 ATGAAAAAGAGTAATATGCTTTAGACGCTGATGTAATTTACGATTACAGGATAATAAGCATTAGCA 60
DB 241 ATGACTTCGGTAATGCTGTTTCGGAGAGATCTTCGAGTAAACGATAATAAGCTCTCTAT 300
QY 61 CACGGTTTACAAAATTCGACGCTGATGTAATTTATTTATTTCCAAATGAATCCTCAA 120
DB 301 CATGC-----TTGTAAGAGAGACGATTTGCTTTTGTATTATTTCAAGTAATCCAGCA 351
QY 121 CAATTTATTCAGAAAGTGCTAATCATAAACGCTTTTTCGAAAGCTTAGCCTCGCTTCAAA 180
DB 352 CAGTTTCATCAGAGAGTCCCTAGCCACCAAGCTTTTTCGAAAGTGCTGCTCATTTTAAG 411
QY 181 GAACGAATCGATCAAGAGGACACATTTACAAATCATGTCGCGCAACCAATTAGATTTATTT 240
|||||

Db 412 CAAGAAATCGATAAAACCTGGCCATTTTACAAATCATGTTTGGTGAAACCGATAGATGCTTC 471
Qy 241 TCAGGTTTGAACCCAAATTTACCCGATTTGGCAGCCATTTTATTTTAAATGAAGTACTTGT 300
Db 472 CAACAACCTTAAAGATTCGCTACCAAGCTGGGATAAAGTTTATTTTCAACCGTGATGAACA 531
Qy 301 GGCTTTGGGGCAAGCGGGACCGCAAGCTATGCGCTTTTGTGAAGAAAATAATATTTCAG 360
Db 532 GGATACGGAGCAAGCGGGATGAGCGCGCGACGCGTCTTTGACGAACAANAATCGAG 591
Qy 361 TCTTTCTCTTTCAAGATGCTATTTGATGCTCTCGAAGAAATTAAGAAGACGATGGC 420
Db 592 GTTCAAGCTTCCACGATAGTATCTTCAITCAGCGGAAGAAAGTAAAGAAATCTCCAAACA 651
Qy 421 AGCAAGTACCAAGTGTTTACGCCCTATTACAAATAATGGAAGAGCGCCTAAAGAAACA 480
Db 652 GAATFACTATAAAATTTTACCCCTTATTATAAAAAATGGCGGGAAGAAATAAAGAAACG 711
Qy 481 CCGATTCTGTTTCTCTATACAGCTGAAAAAATTTTATAGTCGTCTCTTTTCCAGAAGAG 540
Db 712 CCGTTCAAATGACTTTTAAGCATGAGATATCGGAAAGAAAGCTTGTCTCTGAATAT 771
Qy 541 GAACGAGCTTATCGTGAACAGATTCGAGGATTCCTTTAACACACTATAGTGTGGCGAA 600
Db 772 GAAGAACAAATTTGCGGAAATGACT-----AGCGATTTTACCGATATTAGATATTGGTGAA 825
Qy 601 GAAACAGCGAAGCGCTTAAATACTTTTATTTGATCAAAAATCTTCAATCTATGAAT 660
Db 826 CGAGCAGCGAACACGAGACTTGGCAATTTTATTAAACACGATGTGTGACTATGACAAA 885
Qy 661 AAGCGTGATTTCTCTTATCAGATCAACAGAGTCATCTGTCTACTTTTAAAGAACGGGA 720
Db 886 GCGAGAGATTTCCCGGAATCGATTAACAAGCCATTTATCACGTTATTTACGNAACGGGG 945
Qy 721 GAACCTTTGATTCGCACCATTTGGCAAGAGCTTCGATCTGTGCCCTCTAGCTTAAGTAAA 780
Db 946 GAAATCTCGATTCGACGATTTGGCAGACACTTCAAGAAACAGAAAGCAACAGAGGACGA 1005
Qy 781 GAAACCTTCAAAAAGAAATTAGCTTGGCGGACCTTTTACAAATATGATCTATGTCGCTTT 840
Db 1006 GCTACATTTGAAAAGAACTGTGTAGCGCGACTTTTATAATATGATTTACGTTCTCTTT 1065
Qy 841 CCACAACAAAAGAGGAGCTATTCAAGAAAAATTTTCGTTATATTCAATGACACAAATGAC 900
Db 1066 CTTAACCAAAAACAGAGCCGATCAAGAAAAATTTATCGTTTATTTGAATGGAAAAATAC 1125
Qy 901 CCAGAAATGTTTGTCAAGTGGCAAAAAGGGGAGACGGGGTACCCCTATATTTGATGCGGCA 960
Db 1126 CGCGAATATTTCAAAGCGTGGCAAGAGGAAGACTGGTTTCCGCTCGTTGATGCGGCG 1185
Qy 961 ATGGACAACTGAATCAAACTGGTTGGATGACAAATCGCTTTAAGAAATGATTCGCCCTCT 1020
Db 1186 ATGGCCAGTTTGAAGAAACTGGTTGGATGCATTAATCGACTAAGAATGATTTACGGCGTC 1245
Qy 1021 TTTTATGTTAAAATTTTACACATCGATTTGGCGTTGGGTGAAAAATCTTTCAAAAAATG 1080
Db 1246 TTTTAAACAAAGATTTGCTGATTTGATTTGGCGTTTGGCGAAAAGTATTTTCAACAATG 1305
Qy 1081 TTGATTGACTATGATGCTGCCAATAATATCGGTGGCTGGCAATGGGCTCTTCAACAGGA 1140
Db 1306 CTGATTGATTATGATCTGCGAGTAAATTTGTTGGCTGGCAATGGCGGCTTCGACTGGA 1365
Qy 1141 ACGAGCGCTGCTCTTATTTTCGGATTTTAAATCCAAATTTATCCAGTCAAAAAATTTGAT 1200
Db 1366 ACGGATGGGTGCCACTATTAGGATTTTCAACCAACGACACAAATCACAAAAATTTGAT 1425
Qy 1201 AATGAGCGCCAGTTTCATCAAAAATATGTTCCAGACTTTAGCAAGTGCCCAAAAATGAT 1260
Db 1426 TCGACTGGGAAATTTATTTCGAAAATATGTAAGAGATTTAGCGAATCTACCTGATAAATAT 1485
Qy 1261 ATTCAACCAAAATCTAATGAACGAGCCCTTACAAACGCAATATCATGTACATTTAGGA 1320
Db 1486 ATTCATCAACCAAAAATGTCAGAAACTGAGCAGAAAGAGCATGGCTTCTGCTTAGGA 1545

RESULT 8
AB069245_06
Continuation (7 of 31) of AB069245 from base 600001 (Listeria innocua DNA sequence #684.
WP Sequence split into 31 fragments LOCUS AB069245 Accession Abg69245

WP	Fragment Name	Begin	End
WP	AB069245_00	1	110000
WP	AB069245_01	100001	210000
WP	AB069245_02	200001	310000
WP	AB069245_03	300001	410000
WP	AB069245_04	400001	510000
WP	AB069245_05	500001	610000
WP	AB069245_06	600001	710000
WP	AB069245_07	700001	810000
WP	AB069245_08	800001	910000
WP	AB069245_09	900001	1010000
WP	AB069245_10	1000001	1110000
WP	AB069245_11	1100001	1210000
WP	AB069245_12	1200001	1310000
WP	AB069245_13	1300001	1410000
WP	AB069245_14	1400001	1510000
WP	AB069245_15	1500001	1610000
WP	AB069245_16	1600001	1710000
WP	AB069245_17	1700001	1810000
WP	AB069245_18	1800001	1910000
WP	AB069245_19	1900001	2010000
WP	AB069245_20	2000001	2110000
WP	AB069245_21	2100001	2210000
WP	AB069245_22	2200001	2310000
WP	AB069245_23	2300001	2410000
WP	AB069245_24	2400001	2510000
WP	AB069245_25	2500001	2610000
WP	AB069245_26	2600001	2710000
WP	AB069245_27	2700001	2810000
WP	AB069245_28	2800001	2910000
WP	AB069245_29	2900001	3010000
WP	AB069245_30	3000001	3011208

Query Match 36.2%; Score 518.4; DB 6; Length 110000;
Best Local Similarity 61.2%; Pred. No. 5.1e-119;
Matches 878; Conservative 0; Mismatches 541; Indels 15; Gaps 2;

Qy 1 ATGAAAAGAGTAATATATGGTTTACACGCTGATTTACGATTTACAGGATTAACAGGATTAATAAGCATTAGCA 60
Db 28080 ATGACTTCAGTAATATGGTTTTCGTAGAGTCTTCGAGTAAATGATTAATAAGCTCTTTAT 28139
Qy 61 CACGCGTTACAAAATCTGCAGCTGATGAATTCGATTTATTTATTCAAAATGAATCCCTCAA 120
Db 28140 CATGCTCTAAAGA-----AGAGATTTAATTTTGTATTTCAGTAAATCCAGAA 28190
Qy 121 CAATTTATTCAGAAAAGTGCTAATCATACGCTTTTTTTTGCAGCTTAGCTCGTTCAAA 180
Db 28191 CAATTTATCAAGGAAGCCCTAGTCCCAAGCATTTTTTCGCGAGTGTAGCTCATTTTCAA 28250
Qy 181 GAACGAATCGATCAAGAGGACATTTTACAAATCATGTCGGCCAAACCATTAGATTTATTT 240
Db 28251 CAAGAACTAAATAAAAACACCCATTTGCAAAATCATGTTTGGCGAGCCCAATCGAGTCCCTA 28310
Qy 241 TCACGTTTGAACGCAAAATTTACCCGATTTGCGAGCCCATTTTATTTTAAATGAAGATACTTGT 300
Db 28311 AAACAATTAAGAAAAAATACCAACTTGGGATAAAGTTTCTTCAACCCCGATGAACA 28370
Qy 301 GGCTTTGGGCAAGCGGGACCGAGCTATGCGCTTTTTTTTGAAGAAAAATATATTTTCAG 360

Db 28371 GGCTACGAGCGAGTCGAGACGAGCGCTGCCGAGCATCTTTTGTGTGATAAGAAATCACA 28430
Qy 361 TCTTCTCTTTTCAAGATGCGCTATTGTGATGGCTCTGAAGAAATTAAGAAAGACGATGGC 420
Db 28431 GTTCACAGCTATCAGATAGTTACCTTCATTCAGCTGAGAAAGTGAAATAATCCGCCACA 28490
Qy 421 AGCAAGTACCAAGTGTTTTACGCCCTTATTACAAATAATGAAAGAGCGCCCTAAAGAAACA 480
Db 28491 GNAATACTACAAATCTTCACTCTTACTACAAAAATGGCGGAAGAAATAAAGAAATG 28550
Qy 481 CCGATTCCTGTTTCTATACAGCTGAAAAATTTTGTAGTGTGTCTTTTCCAGAGAG 540
Db 28551 CCTTTAAAGTCACCTTTAAACACGAAAAATTTAGGAAAGAAAGCTTATTTCCAAATTAT 28610
Qy 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTAACACACTATAGTGTGCGGAA 600
Db 28611 GAGGAACAGTTTAGAGAACTGATTT-----CAAGATTTTACCAGCGCTTTGATTCGGTGAA 28664
Qy 601 GAAACAGCGCAGAGCGCTTAAATACTTTTATGATCAAAAACTTCAATCCTATGAAAT 660
Db 28665 AAAGCAGCGAATACAGACTTGCAACTTTGTAAAGAAAGATTTAGCAGACTATGACAA 28724
Qy 661 AAGCGTGAATTTCTTATCAGATCAAAACGAGTCACTGTCTACTTTTAAAGAACGGGA 720
Db 28725 GCAAGAGACGTCACGCGCTTGATAAAACGAGTCACTTTATCAAGCTATTTACGAAACGGGA 28784
Qy 721 GAACTTTGATTCGACCACTTTGGCAAGCTTGCATCTGTGCCTTCTAGCTTAAGTAA 780
Db 28785 GAGATTTGATTCGATTCGATTTGGCAGGCACCTTCAAAAAAGAAAGCTTACAGAGGACGA 28844
Qy 781 GAAACCTTTCAAAAAAGAAATAGCTTGGCGCGACTTTTACAAATATGATCTATAGTGCCTTT 840
Db 28845 GCAACATTCGAAAAAGAACTGTGTGGCGCGATTTTATATATGATTTATGTTCTTTT 28904
Qy 841 CCACAAAAAGAGAGAGCTATTCAAGAAAAATTCGTTATATTCAATGACAAAAATGAC 900
Db 28905 CCAAGCAAAAAAATGAGCTTATCAAGAAAAATATCGTTTATTTGAATGGAAAAATAT 28964
Qy 901 CCAGAAATGTTGTCAGTGGCAAAAGGGGAGCGGGTACCCTATTAATTTGATGCCGCA 960
Db 28965 CGCGAAATTTTCAAGAAGTGGCAAGCGGCAAACTGTTTTTCCGCTTGTGATGCTGCG 29024
Qy 961 ATGCAGCAACTGAATCAAACTGGTTGGATGCACAATCGCTTAAGAAATGATTACTGCGCTCT 1020
Db 29025 ATGCCCAATTAAGAGACGGCGCTGGATGCATAATCGCGTAAAGATGATCAGCGCTCC 29084
Qy 1021 TTTTGTAGTTAAAAATTTACATCGAATGGCGTTGGGGTGAAAAATACTTTCAAAAAATG 1080
Db 29085 TTTTAAACGAGGATTTACTAATGATTGGCGTTTGGCGRAAATAATTTCAACAAATG 29144
Qy 1081 TTGATTTGACTATGATGCTGCCAATAATATCGGTGCTGCGCAATGGGCTGCTTCAACAGGA 1140
Db 29145 CTAATTGATTACGACCCAGCAGTAAATATTTGGCGTTTGGCAGTGGCGGCTTCGACTGGA 29204
Qy 1141 ACGGAGCTGTCCCTTATTTTCGGATTTTATCCAAATATCCAGTCAAAAAATTTTGCAT 1200
Db 29205 ACAGATGCAAGTACCGGATTTTATAGAAATTTTATCCAAACCAACCAATCGGAAAAATTTGAT 29264
Qy 1201 AATGACGGCCAGTTCAATCAAAAAATATGTTCCAGAACTTTAAGCAAGTGCACAAAGTAT 1260
Db 29265 CCAGATGGTACATTTTATTCGGAATAATATGTAAGGAATTTACGGGACTTGCCGGATAATTC 29324
Qy 1261 ATTTCATCAACCAATCTAATGAACGAGCCTTTACAAACGAATATCATGTACATTTAGGA 1320
Db 29325 ATTCATCAACGAGAAAAATGTGAAACAGAGCAAAAAAGAGCAGTGGTTTGTATTTTAGGA 29384
Qy 1321 GAAATTTATCCAAACCCATTTGCGATTATGATCAAGTAAAAAAACAACATTTGTTCTA 1380
Db 29385 AAAGATTATCCGCTTCCGATAATTCGACCAATAAGAGCGGACGAAAAATAGCGATTCGCGGA 29444
Qy 1381 TATGAAGCCGCAAGAAATTCATCAAGAAATGAACAATCCCAAGGTTTCAATAA 1434
Db 29445 TATGATTTAGCAAGAGGCAATTTCTAGGGGAATATATATGATTAATGAATCAATCA 29498

RESULT 9

ABQ67197_05

Continuation (6 of 12) of ABQ67197 from base 500001 (Listeria innocua contig DNA sequence LOCUS ABQ67197 Accession Abq67197

WP	Fragment Name	Begin	End
WP	ABQ67197_00	1	110000
WP	ABQ67197_01	100001	210000
WP	ABQ67197_02	200001	310000
WP	ABQ67197_03	300001	410000
WP	ABQ67197_04	400001	510000
WP	ABQ67197_05	500001	610000
WP	ABQ67197_06	600001	710000
WP	ABQ67197_07	700001	810000
WP	ABQ67197_08	800001	910000
WP	ABQ67197_09	900001	1010000
WP	ABQ67197_10	1000001	1110000
WP	ABQ67197_11	1100001	1163020

Query Match 36.2%; Score 518.4; DB 6; Length 110000;
Best Local Similarity 61.2%; Pred. No. 5.1e-119;
Matches 878; Conservative 0; Mismatches 541; Indels 15; Gaps 2;

Qy 1 ATGAAAGAGTAATATGGTTTACAGCTGATTTAGGATACAGGATTAAGCAATTAGCA 60
Db 37815 ATGACTTCAGTAATGTGGTTTCGTAGAGATCTTTCGAGTAATGATAATAAAGCTCTTTAT 37874
Qy 61 CAGCGTTACAAAATTCGCGAGCTGATGAATTTGATTTTATTTTCCAAATGAATCCCTCAA 120
Db 37875 CATGCCCTGAAGA-----AGAAGATTTAATTTTGTATTTTCAAGTAAATCCAGAA 37925
Qy 121 CAATTTATCAAGAAAGTGTAAATCATACAGCTTTTTTTTGCAGCTTAGCTCTGTTCAA 180
Db 37926 CAATTTATCAAGGAAGCCCTAGTCACCAAGCATTTTTCGGAGTGTAGCTCATTTTCAA 37985
Qy 181 GAACGAATCGATCAAGAGGCACATTTTCAAAATCATGTGCGCGAACCATTAGATTTATTT 240
Db 37986 CAAGAACTAAATAAAAAACACCCATTTGCAAAATCATGTTTGGCGAGCCAATCGAGCTCCTA 38045
Qy 241 TCAGTTTGAACCGCAATTTACCGGATTTGGCAGGCCATTTATTTTAAATGAAGTACTTGT 300
Db 38046 AAACAATTAAGAAAAAATAACCAACTTGGGATAAAGTTTCTTCAACCGCGATGAACA 38105
Qy 301 GGCTTTGGGCAAGCGGACCCAGCAAGCTATGGCTTTTGTGAAGAAAAATAATTTCAG 360
Db 38106 GGCTACGAGCGATCGAGAGCGGCTGCCGAGCATCTTGTCTGATAGGAATCACA 38165
Qy 361 TCTTCTCTTTTCAAGATGCTTATTTGCTATGGCTCTCAAGAAATTAAGAAAGACGATGGC 420
Db 38166 GTTCACAGCTATCAGATAGTTACCTTTCAGCTGAAGAAAGTGAATAATCCGCCACA 38225
Qy 421 AGCAAGTACCAAGTGTTTAGCCCTTATACAAATATGGAAGAGCGCCCTAAAGAAACA 480
Db 38226 GAATACTACAAAATCTTCACTCTTACTACAAAAAATGGCGGAAGAAATAAAGAAATG 38285
Qy 481 CCGATTCTCTTCTTATACAGCTGAAAAAATTTTATAGTGGCTGTCTTTTCCAGAAAGAG 540
Db 38286 CCTTTAAAGTCACTTTTAAACCCAGAAAAAATTAGGAAGAAAGCTTATTTCCAAATAT 38345
Qy 541 GAACAGCTTATCGTGAACAGATTTGCGAGGATTCCTTTTAAACACTATAGTGTGCGGAA 600
Db 38346 GAGAAACAGTTTAGAAGACTGATTT-----CAAGATTTTACCAGCTTTGATTTCCGGTGA 38399
Qy 601 GAAACAGCGAAGCGCGCTTAAATATCTTTTATGATCAAAAACTTCAATCTCTATGAAT 660
Db 38400 AAAGCAGGAATACGAGACTTGCAAACTTTGTAAAGAAAGATTTAGCAGACTATGACAAA 38459
Qy 661 AAGCGTGAATTTCTTATCAGGATCAACGAGTCACTGTCTACTTTTTTAAAGAACGGGA 720
Db 38460 GCAAGAGACGTCGCCAGCGCTTTGATAAAGCAGTCAITTTATCACGCTATTTACGAACGGGA 38519
Qy 721 GAACTTTTCGATTCGCACCATTTTGGCAAGAGCTTGCATCTGTGCTTCTTAGCTTAAGTAAA 780

Db	38520	GAGATTTTCGATTCGTACGTTTGGCAGCACCTTCAAAAAGAGAGCTACAGAGACGA	38579
Qy	781	GAACCTTTCAAAAAGAAATAGCTTGGCGGACCTTTTACAAATATGATCTATAGTGGCTTT	840
Db	38580	GCAACATTCGAAAAAGAACTGTGTGGCGGATTTTATAATATGATTTATGTTCTCTTT	38639
Qy	841	CCACAAACAAAAGAGGAGCTATTCAAGAAAAATTTTCGTTATATTCAATCGCAAAATGAC	900
Db	38640	CCAAAGCAAAAAATGAGCCTATTCAAGAAAAATTTATCGTTTATTGAATGGGAAAAATAT	38699
Qy	901	CCAGAAATGTTTCAAGTGCACAAAAAGGAGACGGGTACCCCTATAAATGATGCGCA	960
Db	38700	CGCGAATTTTCAAGAAGTGCACAGCGGCAAACTGTTTTCCGTTGTCGATGCTGCG	38759
Qy	961	ATGCGACAACTGAATCAAACTGGTTGGATGCACAAATCGCTTAAAGAAATGATTTACTGCTCT	1020
Db	38760	ATGCGCCAAATTAAGAGACGGGCTGGATGATTAATCGGCTAAGAAATGATCACGGCTTC	38819
Qy	1021	TTTTTAGTTAAAAATTTACACATCGATTTGGGTTGGGGTGAAAAATACTTTCAAAAAATG	1080
Db	38820	TTTTTAACGAAGGATTTTACTAAATTTGATTTGGCGTTTTCGCGAAAAATATTTTCAACAAATG	38879
Qy	1081	TTGATTCGACTATGATGCTGCCAAATAATATCGTGGCTGGCAATGGGCTGCTTCAACAGGA	1140
Db	38880	CTAATTTGATTACGACCCAGCGAGTAATATTGGCGGTTTGGCAGATGGCGGCTTCGACTGGA	38939
Qy	1141	ACGGACGCTGCTTCCTTATTTTCGGATTTTAAATCCAATTTATCCAGTCAAAAAATTTGAT	1200
Db	38940	ACAGATCGATACCGTATTTTATAGAAATTTTAAATCCAACCACTCGGAAAAATTTGAT	38999
Qy	1201	AATGACGCCAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCCACAAAAGTAT	1260
Db	39000	CCAGATGGTACATTTATTCGGAATATGTAAGGAATTTACGGGACTTTGCGGGATAATTC	39059
Qy	1261	ATTTCATCAACCAATCTAATGAACGAAGCCCTTACAAAGCAATATCATGTACATTTTAGGA	1320
Db	39060	ATTTCATCAACAGAAAAATTTCTGAAACAGACAGACAAAAAGAGCATGTTGATTTTAGGA	39119
Qy	1321	GAATAATTATCAAAACCCATTGTCGATTTATGCATCAAGTAAAAACAAACATTTGTTCTA	1380
Db	39120	AAAGNTTATCCGTTCCGATAATCGACATAAAGAGCGAGAAATTTAGCGATTGCGCGA	39179
Qy	1381	TATGAGCGGACGAAGAAATTCATCAAGAAATGAACAAATCCAGGTTTCAATAA	1434
Db	39180	TATGAGTTTACGAAGGAGCATTTCTAGGGGAATATATAGATAATGAATCAATCA	39233

RESULT 10

ABA03041_06

Continuation (7 of 30) of ABA03041 from base 600001 (Listeria monocytogenes EGD-e genome)

WP Sequence split into 30 fragments LOCUS ABA03041 Accession ABA03041

Fragment Name	Begin	End
ABA03041_00	1	110000
ABA03041_01	100001	210000
ABA03041_02	200001	310000
ABA03041_03	300001	410000
ABA03041_04	400001	510000
ABA03041_05	500001	610000
ABA03041_06	600001	710000
ABA03041_07	700001	810000
ABA03041_08	800001	910000
ABA03041_09	900001	1010000
ABA03041_10	1000001	1110000
ABA03041_11	1100001	1210000
ABA03041_12	1200001	1310000
ABA03041_13	1300001	1410000
ABA03041_14	1400001	1510000
ABA03041_15	1500001	1610000
ABA03041_16	1600001	1710000
ABA03041_17	1700001	1810000
ABA03041_18	1800001	1910000
ABA03041_19	1900001	2010000

WP	ABA03041_20	2000001	2110000
WP	ABA03041_21	2100001	2210000
WP	ABA03041_22	2200001	2310000
WP	ABA03041_23	2300001	2410000
WP	ABA03041_24	2400001	2510000
WP	ABA03041_25	2500001	2610000
WP	ABA03041_26	2600001	2710000
WP	ABA03041_27	2700001	2810000
WP	ABA03041_28	2800001	2910000
WP	ABA03041_29	2900001	2944528

Query Match

Best Local Similarity

Score 516.8; DB 6; Length 110000;

Pred. No. 1.3e-118;

Matches 877; Conservative 0; Mismatches 542; Indels 15; Gaps 2;

Qy	1	ATGAAAGAGTAAATATGTTTATAGCTGATTTACAGATTACAGATTAAAGCAITTAGCA	60
Db	29088	ATGACTTCTGTAATGTGTTTCGGAGAGATCTTCGAGTAAATGATAATAAAGCCCTTAT	29147
Qy	61	CACGCTTACAAAATTTCTGCAGCTGATGAATTGATTTTATTTCCAAATGAATCCTCAA	120
Db	29148	CATGC-----TTGTAAGAGGACGATTTGCTTTTGTATTTCAGTAAATCCAGCA	29198
Qy	121	CAATTTATTCAAGAAAGTGTAAATCATAACGCTTTTTTTTGCAGAGCTTAGCTCGTTCAA	180
Db	29199	CAGTTTCATCACAGGAAGTCTTAGCCACCAAGCTTTTTTTTGCAGTGTGCTCATTTAAG	29258
Qy	181	GAACGAATCGATCAAGAGGACATTTTACAAATCATCTGTCGGCGAACCATTAGATTATT	240
Db	29259	CAAGAAATGTATAAAACCGCGCTTTTACAAATCATCTTTTGGTGAACCGGTAGAAATCT	29318
Qy	241	TCAGCTTTGAAACGCAAAATACCCGATTTCGAGGCCATTTATTTTAAATGAAGTACTTG	300
Db	29319	AAACAATTTAAAGAAACCGCTACCAAGCTGGGATAAAGTTTATTTCACCGCGATGAACA	29378
Qy	301	GGCTTTGGGCGCAAGGGGACCAAGCAAGCTATGCGCTTTTTTTTGAAGAAAAATATATT	360
Db	29379	GGTTACGGAGCAGAGCGGAGCGAGCGGCGGAAAACTTTCTTTGACGAAACAGAAATAG	29438
Qy	361	TCCTTCTCTTTTCAAGATGCCCTATTGTCATGGCTCTGAAAGAAATTAAGAAAGCATGG	420
Db	29439	GTTTCAAGCCTTCCACGACAGCTACCTTCACCTCAGCAGAAAGAGTAAAAAAATCCCC	29498
Qy	421	AGCAAGTACCAAGTGTTTACGCCCTATTACATAAATGGAAGAGGCGCTTAAGAAACA	480
Db	29499	GAATACTACAAAATCTTTTACCCCTTACTATAAAAAATGGCGTGAAGAAATTAAGAAAC	29558
Qy	481	CCGATTCTCTGTTTCTCTATACAGCTGAAAAAATTTTTTAGTGCCTGCTTTTTTCCAGA	540
Db	29559	CCGTTCAAAGTGACTTTTAAAGGCAGATAATATACGAAAGAAAGAACTTATTTCCAAA	29618
Qy	541	GAAGCAGCTTATCGTGAACAGATTGCGAGATTCTCTTTTAAACACACTATAGTGTGGG	600
Db	29619	GAAGAACAGTTCGCGAAATGACTTCGGATTTGCGGATATTAGATTCT-----GGTGA	29672
Qy	601	GAACAGCCAGAGGCGCTTTAATACTTTTATGATCAAAAACCTTCAATCTCTATGAAAT	660
Db	29673	AAAACAGCGAAACACAAGACTTCGGAATTTTATTAACACGATGTTGCTGACTATGACAA	29732
Qy	661	AAGCTGATTTTCTCTTATCAGGATCAAAAGAGTCACTCTGCTACTTTTTTAAAGACGG	720
Db	29733	CGAGAGATTTTCCAGAACTGGNATAAAGAGCCATTTATCGCTATTATACGACAGGA	29792
Qy	721	GAACTTTTCGATTCGCACCAATTTGGCAAGCTTTGCAATCTGTGCTTCTAGCTTAAAGTAA	780
Db	29793	GAAATCTCGGTTCCGACGATTTTGGCAGGCACCTTCAAGAAAAACGAAGCTACAGAAG	29852
Qy	781	GAACCTTCAAAAAGAAATTAGCTTCGGCGCACTTTTACAAATATGATCTATAGTGGCTT	840
Db	29853	GCCATATTGAAAAAGAGCTTTGTTGGCGTGACTTTTATATAATGATGATTATGTTCTTT	29912
Qy	841	CCACAACAAAAAGAGGAAGCTATTTCAGAAAAAATTTTCGTTTATATTCAATGACAAATG	900

Db 29913 CCTAACCAAAAACGAGCCTATCAAGAAATATTATCGTTTATTAATGGAAGAAACAAC 29972

Qy 901 CCAGAAATGTTTGTCAAGTGGCAAAAAGGAGAGACGGGTACCTATTAATGATGCCGCA 960

Db 29973 CGCGAATTTTCAAGACATGGCAAGAGGAGACGTGTTTCCGCTCGTTGATGCGACG 30032

Qy 961 ATGCAGCAATCAATCAAACTGGTTGGATGCACAACTGCTTAAAGAAATGATTACTGCTCT 1020

Db 30033 ATGCCCACTGAAAGAACTGGTTGGATGCATATCAATCAATTAAGATGGTTACGGCTCC 30092

Qy 1021 TTTTGTAGTTAAAAATTTACACATCGATTGGCGTTGGGTGAAAAATATCTTCAAAAAATG 1080

Db 30093 TTTTACGAAAGACTTGTCTGATTGATGGCGATTGGGGAATAATATTTTCAACAATG 30152

Qy 1081 TTGATTGACTATGCTGCCAATATATCGTGGCTGGCAATGGCTGCTTCAACAGGA 1140

Db 30153 CTGATTGATTATGATCTCGAGTAAATATGTTGGCTGGCAATGGCGGCTTCGACTGGA 30212

Qy 1141 ACGGAGCTGCTCCCTTATTTTCGGATTTTAAATCCAATTTATCCAGTCAAAAAATTTGAT 1200

Db 30213 ACAGATGCGGTGCCATCTTTAGGATTTTCAACCCACGACACATCAAAAAATTTGAT 30272

Qy 1201 AATGACGCGCAGTTTCATCAAAAAATATGTTCCAGAACTTTAAGCAAGTCCCAAAAGTAT 1260

Db 30273 CCGACGGGGAATTTATTCGAAATATGTAAGAGATTAGCGAATTTACCTGATAAATTC 30332

Qy 1261 ATTCAATCAACCAATCTAATGAACGAGCCTTACAAACGCAATATCATGTATCATTTAGGA 1320

Db 30333 ATTCATCAACCAAGAAAAATGTCAGAAATAGAGCAGAAAGATATGTTTGTCTATTAGGA 30392

Qy 1321 GAAATATCAACCAACCAATGTCGATTATGATCAAGTAAAGAAACAAACATTTGTTCTA 1380

Db 30393 AAAGACTATCCATTCCTTTAATGACCAATAAGAACGGCGTAAATTTAGCCATTCACGC 30452

Qy 1381 TATGAAGCAGCAAGAAATTCATCAAGAAATGAACAATCCAAAGTTTCAATAA 1434

Db 30453 TAGAGTTAGCAAGAGCATTTAGGGGAATATATAGACAATGAGTCAATCA 30506

RESULT 11

ID ABQ68877 standard; DNA; 1451 BP.

XX AC ABQ68877;

XX AC ABQ68877;

XX AC ABQ68877;

DT 29-AUG-2003 (revised)

DT 29-AUG-2002 (first entry)

XX DE Listeria monocytogenes 4b contig DNA sequence #1643.

XX Antibacterial; Listeria; food contamination; mutational analysis;

KW infection; ds.

XX Listeria monocytogenes ATCC 19115.

OS W0200228891-A2.

XX 11-APR-2002.

XX 04-OCT-2001; 2001WO-FR003061.

XX 04-OCT-2000; 2000FR-00012697.

XX (INSP) INST PASTEUR.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Kunst F, Glaser P;

XX WPI; 2002-332479/37.

XX New genomic sequences from Listeria species, useful for detection,

PT treatment and prevention of infection, also related polypeptides,

PT antibodies and modulators.

XX Claim 14; SEQ ID NO 1690; 180pp; French.

XX The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 1451 BP; 443 A; 308 C; 327 G; 373 T; 0 U; 0 Other;

Query Match 29.1%; Score 416.8; DB 6; Length 1451;

Best Local Similarity 59.0%; Pred. No. 3.7e-94;

Matches 759; Conservative 0; Mismatches 512; Indels 15; Gaps 2;

Qy 1 ATGAAAAGCTAATATGTTTAGACGTGATTACGATTACAGGATAATAAAGCATTAGCA 60

Db 39 ATGACTTCGGTAATGTGTTTCGGAGAGATCTTCGAGTAAACGATAATAAAGCTCTCTAT 98

Qy 61 CACGCGTTACAAAATCTGCAGCTGATGAATGATTTTATTTATTTCCAAATGAATCTCAA 120

Db 99 CATGC-----TTGTAAGAGGACGATTTGCTTTGTTTATTTCAAGTAAATCCAGCA 149

Qy 121 CAATTTATTCAGAAAAGTCTAATCATACGCTTTTTTTTGCAGCTTTAGCCTCTGTTCAA 180

Db 150 CAGTTTCATCAGGAAAGTCTTAGCCACCAAGCTTTTTTTGCAAGTGGCTCATTTTAAAG 209

Qy 181 GAACGAATCGATCAAGAGGACATTTCAATCATGTCGCGCAACCATTAAGATTTATTT 240

Db 210 CAAGAAATTCGATAAAATCTGCGCATTTTACAAATCATGTTTGTGAAACCATTAAGATGCTTC 269

Qy 241 TCACGTTTGAACGCAAAATTTACCGGATTGGCAGGCCATTTATTTTAAATGAAGATACCTGT 300

Db 270 CAACAATTAAGATTTCGTACCAAGCTGGGATAAAGTTTATTTTCAACCGTGAAGAAACA 329

Qy 301 GGCTTTGGGCAAAAGCGGACAGCAAGCTATGCGCTTTTTTTTGAAGAAAATAATATTGCG 360

Db 330 GGATACGAGCAAAAGCGGATGAGCGCGCAAGCTTTCTTTGACGAACAAAAAATTCGAG 389

Qy 361 TCTTTCTCTTTTCAAGATGCTTATTTGCATGGCTCTGAAGAAATTAAGAAACGATGGC 420

Db 390 GTTCAAGCTTTCCACGATAGCTATCTTCAATTCAGCGGAAGAAAGTAAAGAAATCTCCAAACA 449

Qy 421 AGCAAGTACCAAGTGTTTTACGCCCTTATTAATAATGGAAGAGCGCCCTAAAGAAACA 480

Db 450 GAATACTATAAATTTTTTACCCCTTATTAATAAATGCGCGGAAGAAATTAAGAAACG 509

Qy 481 CCGATTCTCTGTTTCTCTATACAGCTGAAAAATTTTTTGTGCGTGTCTTTTCCAGAAAG 540

Db 510 CCGTTCAAAGTGACTTTTAAAGCATGAGAAATATCGGAAAGAAAGCTTGTCTCTGAAATAT 569

Qy 541 GAAGCAGCTTATCGTGAACAGATTGCGAGGATTCCTTTTAAACACTATAGTGTCCGCGAA 600

Db 570 GAAGAAACAATTTGCGGAAATGACT-----AGCGATTTTACCGATATTAGATATTGTTGAA 623

Qy 601 GAAACAGCCAGAGCGCTTAAATACTTTTATGATCAAAAACTTCAATCTCTATGAAAT 660

Db 624 CGAGCAGGAAACACGAGACTTTCGGAATTTTATTAACACGATGTTGCTGACTATGACAAA 683

Qy 661 AAGCGTGATTTTCTTTATCAGGATCAAAACGAGTCAATCTGTCTACTTTTTTAAAGACGGGA 720

Db 684 CGGAGAGATTTCCCGGAATCGATAAACAAGCCATTTATCACGTTATTTTACGAACGGGG 743

Qy 721 GAATCTCGATTCGACCATTTGGCAAGAGCTTGCATCTGTCCCTTCTAGCTTAAGTAA 780

Db 744 GAATCTCGATTCGACCATTTGGCAGACACTTCAAGAAACAGAAAGCAAGAGACGA 803


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QY 669 TTTTCCTTATCAGGATCAACAGAGTCATCTGTCTACTTTTTTTAAAGACGGAGAACTTTC 728
Db 696 TTTTCACGGCAGCTAGGACAGAGTCGGTGTCTCTCTTTTTTAAGATAGAGCTATTGG 755
QY 729 GATTCCGACCATTTGGCAAGAGCTTGCATCTGTGCTTCTAGCTTTAAGTAAAGAAACCTT 788
Db 756 CATTCGACGGTATATCACGCTGTGCGTCAAGCACCAATAGTCTAGGCGAAGCTACTTT 815
QY 789 CAAAAAGAAATTAGCTTGGCGGACCTTTTACATATGATCTATAGTGGTTTCCACACA 848
Db 816 TTTTAAAGAAATTAGCTTGGAGAGACTTTTACAATATGCTATGTGGCTTATCTCTGATCA 875
QY 849 AAGAGAGNAGCTATTTCAGAAABAAATTCGTTTATATCAATGGACAAATGACCCAGAAAT 908
Db 876 GAAAACTCAGCCTATCCAAAAAGCCCTTTTCTCAAAATCGAATGGGTTAATATCTGACTG 935
QY 909 GTTTCGCAAGTGGCAAAAGGGGAGACGGGTACCTTATAATTGATGCGCAATGCGACA 968
Db 936 GTTTCAGTTGTGGAAGAGGTAAACGGGTACCTTATGTCGATGCTGCAATGCTTCA 995
QY 969 ACTGAATCAAACTGTGTGATGCAACAATCGCTTAAAGATGATTAAGTCTCTTTTAACT 1028
Db 996 GTTACAAAGACAGGATGATGCATAATCGTTTACGAATGATAGTAGCTTCTTTTAAAC 1055
QY 1029 TAAAAATTTACACATCGATTGGCGTTGGGTGAAAAATACTTTCAAAAAATGTTGATTGA 1088
Db 1056 TAAAGATCTTTATGTGATTGGCGTTTAGGAGAGCAGTATTTTCAACAACTAATTTGA 1115
QY 1089 CTATGATGCTGCAATATATCGGTGGCTGGCAATGGGCTGCTTCAACAGGAACGGAGCG 1148
Db 1116 TTATGATGCTGCAGTATATCGGAGGATGGCAGTGGGCTGCTTCCACTGGAAACAGATGC 1175
QY 1149 TGTCCCTTATTTTCGGATTTTAAATCCAAATATATCCAGTCAAAAAATTTGATAATGACGG 1208
Db 1176 TGTTCCTTATTTTGAATATTTAAATCTCTTACTCAAGTAAAGCGCTTTGATCCTTAAAGG 1235
QY 1209 CAGTTTCATCAAAAAATATGTTCCAGAACTTAAGCAAGTGCACAAAGTATATTCATCA 1268
Db 1236 CGAGTTTATTAAGCGGTATTTGGCTCACTAGAACACGTTCCAGAGAAAGTATCTCCAGA 1295
QY 1269 ACCAAATCTAATGACGAAGCCTTACAAACGCAATATCATGTATCATTTTAGGAGAAAAATTA 1328
Db 1296 ACCGTGGAAGATGCCAAAAAACCTTCAAGAGAGTGTCTGTATTTATGTCACAGACTA 1355
QY 1329 TCCAAACCCATTTGCGATTATGTCATCAAGTAAAAAACAACATTTGTTTCTATATGAAGC 1388
Db 1356 TCTCAACCAATTTGTCATCATGCTAAACACGCTGAACAGCTATTGCAAAAGTATGATG 1415
QY 1389 GAGCAAGAAA 1399
Db 1416 GCAAAAAGAAA 1426
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RESULT 13

ADP03864

ID ADP03864 standard; DNA; 1446 BP.

XX

AC

ADP03864;

XX

12-FEB-2004 (first entry)

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DE

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KW

XX

OS

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PN

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PD

XX

PF 05-APR-2000; 2000US-00543681.

XX

PR 09-APR-1999; 99US-0128706P.

XX

PA (GENO-) GENOME THERAPEUTICS CORP.

XX

PI Breton GL;

XX

XX WPI; 2003-895291/82.

XX

XX P-PSDB; ADF08036.

DR

XX

XX New Proteus mirabilis polypeptides and polynucleotides, useful as

PT reagents for diagnosis of bacterial disease, as components of

PT antibacterial vaccines, as targets for antibacterial drugs, or as

PT biocontrol agents for plants.

XX

PS Disclosure; SEQ ID NO 4149; 870pp; English.

XX

XX The invention relates to new Proteus mirabilis polypeptides and

CC polynucleotides. The invention also relates to antibodies against the

CC polypeptides, methods for producing the polypeptides, a method of

CC generating vaccines for immunising an individual against P. mirabilis, a

CC method for evaluating a compound for the ability to bind a P. mirabilis

CC polypeptide and a method for screening test compounds for anti-bacterial

CC activity. The polypeptides and polynucleotides are useful as molecular

CC targets for diagnosing, preventing and treating pathological conditions

CC resulting from bacterial infection, as reagents for diagnosis of

CC bacterial diseases, as components of antibacterial vaccines, as targets

CC for antibacterial drugs or as bio-control agents for plants. This

CC sequence represents a Proteus mirabilis polynucleotide of the invention.

XX

SQ Sequence 1446 BP; 418 A; 321 C; 287 G; 420 T; 0 U; 0 Other;

Query Match 14.8%; Score 212.2; DB 10; Length 1446;

Best Local Similarity 60.0%; Pred. No. 7.9e-43;

Matches 418; Conservative 0; Mismatches 258; Indels 21; Gaps 3;

QY 596 GCGAAGAAAACAGCCAGAGCGCTTAAATACTTTTATTGATCAAAAACTTCAATCCTATG 655

Db 635 GCGAACAAGCAGCGTTACAGCGTTTAAACAGTTTTGCTATGAAAGGGTGATACATTATG 694

QY 656 AAAATAAGCGTGATTTTCTTATCAGGATCAAAACGAGTCATCTGTCTACTTTTTTAAGAA 715

Db 695 CAAAATGCGAGATATTCCTGTATTGATGAAACCGACTTATATCTCTTATCTTGGCA 754

QY 716 CGGGAGAATTTTCGATTCGCACCATTTGGCAAGAGCTTGC---ATCTGTCCTCTAGCT 772

Db 755 TAGGCCTAGTGTGTGCGCAATGTTTTTAATCGCCTTTACCAACAGAGCCTGATTTCT 814

QY 773 TAAGTAAAGAAAACCTTCAAA-----AAAGAAATTAGCTTTGGCGCGACTTTT 817

Db 815 TAGAAAATAACCATTCAGTGCATTTGTTGTTTAAATAGTTAGTTTGGCGCGAGTTT 874

QY 818 ---ACAATATGATCTATAGTGGTTTCCAAACAAAAGAGAGAGCTATTCAAGAAAAAT 874

Db 875 ATCAACATCTAATAGTTGCTAAACCGAGTTTATCCAAACAGATAGCTTTTCAACCATGGA 934

QY 875 TTCGTTATTTCAATGGCAAAATGACCCAGAGAAATGTTTGTCAAGTGGCAAAAAGGGAGA 934

Db 935 CAGAAAATATTTGCGTGGCGTAAATGACCAAACTGAATTTACCCCTTGGACACAGGGCTTAA 994

QY 935 CGGGGTACCTTATTAATTGATGCGCAATGCGCAAACTGAATCAAACTGGTTGGATGCACA 994

Db 995 CAGGCTTTCTTATTTATGATGCGCGATGCGCAACTGAATCAAAACCGCTGATGCACA 1054

QY 995 ATCGCTTAAAGATGATTAAGTCTGCTCTTTTATAGTTTAAAAATTTACATCGATTGCGGT 1054

Db 1055 ATCGCTTACGATGCTGACGCGCAAGTTTTTTAGTCAAAAGATCTAATTAATTGATGCGCT 1114

QY 1055 GGGGTGAAAAATACCTTTCAAAAAATGTTGATTTGACTATGATGCTGCCAATATATCGGTG 1114

Db 1115 GGGGGGAAAAATTTATTTTATGTACAAATTAATTTGATGTTGCGTTCGCAAAATATGTTG 1174

QY	1115	GCTGCAATGGCTGCTTCAACAGGACGGACGCTGCTCCCTATTATTTTCGGATTTTAAATC	1174
Db	1175	GCTGCAATGGCTGCTTCAACAGGACGCTGCTGCTCCCTATTATTTTCGGATTTTAAATC	1234
QY	1175	CAATTTATCCAGTCAAAAAAATTTGATTAATGACGCCAGTTTCATCAAAAAAATATGTTCCAG	1234
Db	1235	CGACAACCCAGGACGTAAGTTTGATCTGATGGTGAATTCGCCCACTGGCTACCAG	1294
QY	1235	AACCTAAGCAAGTCCCAACAAAGTATATTCATCAACC	1271
Db	1295	AGCTTGTGCTGATGTCACGATCGCTATATCCATACTCC	1331
RESULT 14			
ACF74095	ID	AAV74095 standard; DNA; 1389 BP.	
XX	AC	ACF74095;	
XX	AC	ACF74095;	
XX	DT	20-NOV-2003 (first entry)	
XX	XX	Staphylococcus aureus DNA #1775.	
XX	DE	Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;	
XX	KW	enzymatic assay; antibiotic target; gene; ds.	
XX	KW	Staphylococcus aureus.	
XX	OS	WO200294868-A2.	
XX	PN	28-NOV-2002.	
XX	PD	27-MAR-2002; 2002MO-IB002637.	
XX	PF	27-MAR-2001; 2001GB-00007661.	
XX	PR	(CHIR-) CHIRON SPA.	
XX	PA	Maignani V, Mora M, Scarselli M;	
XX	PI	WPI; 2003-120786/11.	
XX	DR	P-PSDB; ABM72535.	
XX	DR	New Staphylococcus aureus protein, useful as a vaccine for treating or	
XX	PT	preventing Staphylococcal infection, specifically an infection caused by	
XX	PT	S. aureus, e.g. sepsis.	
XX	PS	Claim 6; SEQ ID NO 3549; 49pp; English.	
XX	CC	The invention relates to novel genes and encoded proteins from	
XX	CC	Staphylococcus aureus. A composition comprising the S. aureus protein, a	
XX	CC	nucleic acid encoding the protein, or an antibody to the protein, is	
XX	CC	useful as a pharmaceutical, particularly as a vaccine for treating or	
XX	CC	preventing infection due to Staphylococcus bacteria, specifically an	
XX	CC	infection caused by S. aureus. The composition is particularly useful for	
XX	CC	treating or preventing sepsis in a patient. The composition can also be	
XX	CC	used for diagnostics. The protein is also used in an assay for enzymatic	
XX	CC	studies and as a target for antibiotics. This sequence represents one of	
XX	CC	the novel S. aureus genes of the invention	
XX	SQ	Sequence 1389 BP; 471 A; 210 C; 261 G; 447 T; 0 U; 0 Other;	
Query Match 14.4%; Score 206.2; DB 8; Length 1389;			
Best Local Similarity 56.2%; Pred. No. 2.5e-41;			
Matches 432; Conservative 0; Mismatches 328; Indels 9; Gaps 12;			
QY	627	TTTTATTGATCAAAACTTCAATCCATGAAATAAGGTGATTTTCTTATCAGGATCA	686
Db	618	TTTTTTAGATCAAGATATACAGAAATACGAACGGGAGAGACTATTACCTGAATTT	677
QY	687	AACGAGTCATCTGCTACTTTTAAAGAACGGGAGAACTTTTCGATTCGCACCATTTGGCA	746
Db	678	AACAAGTCAGCTAAGTGTGCTTTAGCATATGATATTATGAAATTTTAA	737

QY	747	AGT-----GCTTGCATCTGTCCTTCTAGCTTAAAGTAAAGAACTTCAAAAAAGAAAT	800
Db	738	TGATTTATTGGCCGCTTATGATGAAGTAGGCAAACTATGAAGCATTTTATAGCTGAAT	797
QY	801	AGCTTGGCGGACCTTTTACAATATGATCTATAGTGGGTTTCCACAACAAAAAGAGGAAGC	860
Db	798	CATTTTATAGAGATTTTATATGTTAATGACACAGATATCTTGAAACCTCATACCAAGC	857
QY	861	TATTCAGAAAAATTTTCGTTATATTCAATGGACAAATGACCCAGAAATGTTTGTCAAGTG	920
Db	858	TTTCAAAACCTAAATATCGACAGATAAAATGGTCGCAAAATGAAGCGGATTTTAAATGCATG	917
QY	921	GCAAAAAGGGGACGGGTACCTATATGATGCGCAATGCGCACTGAATCAAAAC	980
Db	918	GTGCGAAGGGCAACAGGATTTCCAAATCATTTGATGAGCAATAATGGAATTTGACACAAAC	977
QY	981	TGGTTGGATGCACAAATCGCTTAAAGAAATGATTACTGCTCTCTTTTAAAGTAAATAATTACA	1040
Db	978	TGGTTTATGCATAATCGAATGGAATGGTTGTGCGCAATTTTAAACCAAGATTTATT	1037
QY	1041	CATCGATTGGCGTTGGGGTGAATAATACCTTTCAAAAAATGTTGATTGACTATGATGCTGC	1100
Db	1038	TATAGATTGGACATGGGAGAAAAATTTCTTTAGAAAGCACCTTATTTCATCTATGATGACG	1097
QY	1101	CAATATATCGGTGGCTGGCAATGGCTCTTCAACAGGAACGGACGCTGCTCCCTTATT	1160
Db	1098	ATCAAAATATTCATGGATGGCAATGGCTCTTACAGGTACGGATGCGATGCGGTAAT	1157
QY	1161	TCGGATTTTAAATCCAAATATCCAGTCAAAAAATTTGATAATGAAGCCAGTTCATCAA	1220
Db	1158	TAGATGTTTAAATCCAAATAGACAGAGTGAACGCTTTGATGCTTAAAGCTTTGTATATCAA	1217
QY	1221	AAAAATGTTCCAGAACTTAAGCAAGTGCCACAAGATATTTTCATCAACCAAAATCTAAT	1280
Db	1218	AACATATCTCCGATTTTAAATCAAAATGATGCAAAATATTTGCATGATACA---CAACG	1274
QY	1281	GAACGAAGCTTTACAACGCAATATCATGTACATTTTAGGAGAAAAATATCCAAAAACCAT	1340
Db	1275	CAATGATGCCAACCTTTTGAACAGGGGATTTAGGTAGTCAATTTTAAAGCG	1334
QY	1341	TGTCGATTATGCATCAAGTAAAAAACAACATTTGTTTCTATATGAAGCG	1389
Db	1335	GGTAGATCATCAAGAAAAACGTACACAGTTTATAGCTACATTTTAAAGCG	1383
RESULT 15			
AAV74905	ID	AAV74905 standard; DNA; 1393 BP.	
XX	AC	AAV74905;	
XX	DT	16-MAR-1999 (first entry)	
XX	DE	Staphylococcus aureus contig SEQ ID #594.	
XX	KW	Computer readable medium; vaccine; S. aureus infection; immunodetection;	
XX	KW	cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;	
XX	KW	skin infection; surgical wound infection; scalded skin syndrome;	
XX	KW	toxic shock syndrome; ds.	
XX	OS	Staphylococcus aureus.	
XX	PH	Key Location/Qualifiers	
XX	FT	misc_feature 61..120	
XX	FT	/tag= a	
XX	FT	/note= "these bases represent a line of missing text in	
XX	FT	the sequence listing in the specification. They are	
XX	FT	included to maintain the nucleotide numbering given in	
XX	FT	the specification for this DNA sequence"	
XX	PN	EP786519-A2.	

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